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(54) Title: HUMAN GALACTOKINASE GENE

(57) Abstract

This invention relates to human galactokinase and the identification of galactokinase mutations, a missense and nonsense, as well as isolated nucleic acids encoding same, recombinant host cell transformed with DNA encoding such proteins and to uses of the expressed proteins and nucleic acid sequences in therapeutic and diagnostic applications.

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Human Galactokinase Gene

This invention was made in part with government support under EY-09404
10 awarded by the National Institutes of Health. The U.S. Government has certain
rights in the invention.

Cross-Reference to Related Applications:

This application is a continuation in part of Serial No. PCT/US94/10825,
15 filed 23 September 1994.

Field of the Invention:

This invention relates to human galactokinase and the identification of
galactokinase mutations, a missense and nonsense, as well as isolated nucleic acids
20 encoding same, recombinant host cell transformed with DNA encoding such
proteins and to uses of the expressed proteins and nucleic acid sequences in
therapeutic and diagnostic applications.

Background of the Invention:

25 There are numerous inherited human metabolic disorders, most of which are
recessive. Many have devastating effects that may include a combination of several
clinical features, such as severe mental retardation, impairment of the peripheral
nervous system, blindness, hearing deficiency and organomegaly. Most of the
disorders are rare. However, the majority of such disorders cannot be treated by
30 drugs.

Galactokinase deficiency is one of three known forms of galactosemia. The
other forms are galactose-1-phosphate uridyltransferase deficiency and UDP-
galactose-4-epimerase deficiency. All three enzymes are involved in galactose
metabolism, i.e., the conversion of galactose to glucose in the body. Galactokinase
35 deficiency is inherited as an autosomal recessive trait with a heterozygote frequency
estimated to be 0.2% in the general population (see, e.g., Levy et al., *J. Pediatr.*,
92:871-877 (1978)). Patients with homozygous galactokinase deficiency usually
become symptomatic in the early infantile period showing galactosemia,
galactosuria, increased galactitol levels, cataracts and in a few cases, mental
40 retardation (Segal et al., *J. Pediatr.*, *95*:750-752 (1979)). These symptoms usually
improve dramatically with the administration of a galactose free diet.
Heterozygotes for galactokinase deficiency are prone to presenile cataracts with the

5 onset during 20-50 years of age (Stambolian et al., Invest. Ophthalm. Vis. Sci.,
27:429-433 (1986)).

Galactokinase activity has been found in a variety of mammalian tissues, including liver, kidney, brain, lens, placenta, erythrocytes and leukocytes. While the protein has been purified from *E. coli*, the purification of the protein from 10 mammalian tissues has proven difficult due to its low cellular concentration. In addition, the molecular basis of galactokinase deficiency is unknown.

This invention provides a human galactokinase gene. The DNAs of this invention, such as the specific sequences disclosed herein, are useful in that they encode the genetic information required for expression of this protein. Additionally, 15 the sequences may be used as probes in order to isolate and identify additional members, of the family, type and/or subtype as well mutations which may form the basis of galactokinase deficiency which may be characterized by site-specific mutations or by atypical expression of the galactokinase gene. The galactokinase gene is also useful as a diagnostic agent to identify mutant galactokinase proteins or 20 as a therapeutic agent via gene therapy.

The first clinical trials of gene therapy began in 1990. Since that time, more than 70 clinical trial protocols have been reviewed and approved by a regulatory authority such as the NIH's Recombinant Advisory Committee (RAC), see, e.g., Anderson, W. F., Human Gene Therapy, 5:281-282 (1994). The 25 therapeutic treatment of diseases and disorders by gene therapy involves the transfer and stable insertion of new genetic information into cells. The correction of a genetic defect by re-introduction of the normal allele of a gene has hence demonstrated that this concept is clinically feasible (see, e.g., Rosenberg et al., New Eng. J. Med., 323: 570 (1990)).

30 These and additional uses for the reagents described herein will become apparent to those of ordinary skill in the art upon reading this specification.

Summary of the Invention:

This invention provides isolated nucleic acid molecules encoding human 35 galactokinase, as well as nucleic acid molecules encoding missense and nonsense mutations, which includes mRNAs, DNAs (e.g., cDNA, genomic DNA, etc.), as well as antisense analogs thereof and diagnostically or therapeutically useful fragments thereof.

This invention also provides recombinant vectors, such as cloning and 40 expression plasmids useful as reagents in the recombinant production of human

5 galactokinase proteins, as well as recombinant prokaryotic and/or eukaryotic host cells comprising a human galactokinase nucleic acid sequence.

This invention also provides a process for preparing human galactokinase proteins which comprises culturing recombinant prokaryotic and/or eukaryotic host cells, containing a human galactokinase nucleic acid sequence, under conditions 10 promoting expression of said protein and subsequent recovery thereof of said protein. Another related aspect of this invention is isolated human galactokinase proteins produced by said method. In yet another aspect, this invention also provides antibodies that are directed to (i.e., bind) human galactokinase proteins.

This invention also provides an isolated human galactokinase proteins 15 having a missense or nonsense mutation and antibodies (monoclonal or polyclonal) that are specifically reactive with said proteins.

This invention also provides nucleic acid probes and PCR primers comprising nucleic acid molecules of sufficient length to specifically hybridize to human galactokinase sequences.

20 This invention also provides a method to diagnose human galactokinase deficiency which comprises isolating a nucleic acid sample from an individual and assaying the sequence of said nucleic acid sample with the reference gene of the invention and comparing differences between said sample and the nucleic acid of the instant invention, wherein said differences indicate mutations in the human 25 galactokinase gene isolated from an individual. The sample can be assayed by direct sequence comparison (i.e., DNA sequencing), wherein the sample nucleic acid can be compared to the reference galactokinase gene, by hybridization (e.g., mobility shift assays such as heteroduplex gel electrophoresis, SSCP or other techniques such as Northern or Southern blotting which are based upon the length of 30 the nucleic acid sequence) or other known gel electrophoresis methods such as RFLP (for example, by restriction endonuclease digestion of a sample amplified by PCR (for DNA) or PCR-RT (for RNA)). Alternatively, the diagnostic method comprises isolating cells from an individual containing genomic DNA and assaying said sample (e.g., cellular RNA) by *in situ* hybridization using the DNA sequence of 35 the invention, or at least one exon, or a fragment containing at least 15, preferably 18, and more preferably 21 contiguous base pairs as a probe. This invention also provides an antisense oligonucleotide having a sequence capable of binding with mRNAs encoding human galactokinase so as to identify mutant galactokinase genes.

40 This invention also provides yet another method to diagnose human galactokinase deficiency which comprises obtaining a serum or tissue sample; allowing such sample to come in contact with an antibody or antibody fragment

5 which specifically binds to a mutant human galactokinase protein of the invention under conditions such that an antigen-antibody complex is formed between said antibody (or antibody fragment) and said mutant galactokinase protein; and detecting the presence or absence of said complex.

This invention also provides transgenic non-human animals comprising a
10 nucleic acid molecule encoding human galactokinase. Also provided are methods for use of said transgenic animals as models for disease states, mutation and SAR.

This invention also provides a method for treating conditions which are related to insufficient human galactokinase activity which comprises administering to a patient in need thereof a pharmaceutical composition containing the galactokinase
15 protein of the invention which is effective to supplement a patient's endogenous galactokinase and thereby alleviating said condition.

This invention also provides a method for treating conditions which are related to insufficient human galactokinase activity via gene therapy. An additional, or reference, gene comprising the non-mutant galactokinase gene of the instant
20 invention is inserted into a patient's cells either *in vivo* or *ex vivo*. The reference gene is expressed in transfected cells and as a result, the protein encoded by the reference gene corrects the defect (i.e., galactokinase deficiency) thus permitting the transfected cells to function normally and alleviating disease conditions (or symptoms).

25

Brief Description of the Drawings:

Figure 1 depicts the intron/exon organization of the human galactokinase gene.

Figure 2 is the genomic DNA sequence (and single letter amino acid abbreviations) for human galactokinase [SEQ ID NO: 7]. The bolded DNA sequence corresponds to the exon regions whereas the normal or unbolded type corresponds to the intron regions of human galactokinase.
30

Detailed Description of the Invention:

35 This invention relates to human galactokinase (amino acid and nucleotide sequences) and its use as a diagnostic and therapeutic. The particular cDNA and amino acid sequence of human galactokinase is identified by SEQ ID NO:4 as described more fully below. This invention also relates to the genomic DNA sequence for human galactokinase [SEQ ID NO: 7] and also to mutant human
40 galactokinase genes and amino acid sequences [SEQ ID NO:5 and 6] and their use for diagnostic purposes.

5 In further describing the present invention, the following additional terms will be employed, and are intended to be defined as indicated below.

An "antigen" refers to a molecule containing one or more epitopes that will stimulate a host's immune system to make a humoral and/or cellular antigen-specific response. The term is also used herein interchangeably with
10 "immunogen."

The term "epitope" refers to the site on an antigen or hapten to which a specific antibody molecule binds. The term is also used herein interchangeably with "antigenic determinant" or "antigenic determinant site."

A coding sequence is "operably linked to" another coding sequence
15 when RNA polymerase will transcribe the two coding sequences into a single mRNA, which is then translated into a single polypeptide having amino acids derived from both coding sequences. The coding sequences need not be contiguous to one another so long as the expressed sequence is ultimately processed to produce the desired protein.

20 "Recombinant" polypeptides refer to polypeptides produced by recombinant DNA techniques; i.e., produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide. "Synthetic" polypeptides are those prepared by chemical synthesis.

A "replicon" is any genetic element (e.g., plasmid, chromosome,
25 virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

30 A "replication-deficient virus" is a virus in which the excision and/or replication functions have been altered such that after transfection into a host cell, the virus is not able to reproduce and/or infect addition cells.

A "reference" gene refers to the galactokinase sequence of the invention and is understood to include the various sequence polymorphisms that
35 exist, wherein nucleotide substitutions in the gene sequence exist, but do not affect the essential function of the gene product.

A "mutant" gene refers to galactokinase sequences different from the reference gene wherein nucleotide substitutions and/or deletions and/or insertions result in impairment of the essential function of the gene product such that the levels
40 of galactose in an individual (or patient) are atypically elevated. For example, the G to A substitution at position 122 of human galactokinase [SEQ ID NO: 5] is a

5 missense mutation associated with patients who are galactokinase deficient. Another T for G substitution produces an in-frame nonsense codon at amino acid position 80 of the mature protein. The result is a truncated protein consisting of the first 79 amino acids of human galactokinase.

10 A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

15 A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as 20 well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

25 DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

30 A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

35 A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to 40 eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited

5 by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

"Transfection" or "transfected" refers to a process by which cells take up foreign DNA and integrate that foreign DNA into their chromosome.

10 Transfection can be accomplished, for example, by various techniques in which cells take up DNA (e.g., calcium phosphate precipitation, electroporation, assimilation of liposomes, etc.), or by infection, in which viruses are used to transfer DNA into cells.

15 A "target cell" is a cell(s) that is selectively transfected over other cell types (or cell lines).

A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

20 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature. Thus, when the heterologous region encodes a gene, the gene will usually be flanked by DNA that does not flank the gene in the genome of the source animal. Another example of a heterologous coding sequence is a construct where the coding sequence itself is not found in nature (e.g., 25 synthetic sequences having codons different from the native gene). Allelic variation or naturally occurring mutational events do not give rise to a heterologous region of DNA, as used herein.

30 "Conditions which are related to insufficient human galactokinase activity" or a "deficiency in galactokinase activity" means mutations of the galactokinase protein which affects galactokinase activity or may affect expression of galactokinase or both such that the levels of galactose in a patient are atypically elevated. In addition, this definition is intended to cover atypically low levels of galactokinase expression in a patient due to defective control sequences for the reference galactokinase protein.

35 This invention provides an isolated nucleic acid molecule encoding a human galactokinase protein and substantially similar sequences. Isolated nucleic acid sequences are "substantially similar" if: (i) they are approximately the same length (i.e., at least 80% of the coding region of SEQ ID NO:4); (ii) they encode a protein with the same (i.e., within an order of magnitude) galactokinase activity as the 40 protein encoded by SEQ ID NO:4; and (iii) they are capable of hybridizing under moderately stringent conditions to SEQ ID NO:4; or they encode DNA sequences

5 which are degenerate to SEQ ID NO:4. Degenerate DNA sequences encode the same amino acid sequence as SEQ ID NO:4, but have variation(s) in the nucleotide coding sequences. Hybridization under moderately stringent conditions is outlined below.

Hybridization under moderately stringent conditions can be performed as
10 follows. Nitrocellulose filters are prehybridized at 65°C in a solution containing 6X SSPE, 5X Denhardt's solution (10g Ficoll, 10g BSA and 10g Polyvinylpyrrolidone per liter solution), 0.05% SDS and 100 micrograms tRNA. Hybridization probes are labeled, preferably radiolabelled (e.g., using the Bios TAG-IT® kit). Hybridization is then carried out for approximately 18 hours at 65°C. The filters are then washed in a
15 solution of 2X SSC and 0.5% SDS at room temperature for 15 minutes (repeated once). Subsequently, the filters are washed at 58°C, air-dried and exposed to X-ray film overnight at -70°C with an intensifying screen.

Alternatively, "substantially similar" sequences are substantially the same when about 66% (preferably about 75%, and most preferably about 90%) of the
20 nucleotides or amino acids match over a defined length (i.e., at least 80% of the coding region of SEQ ID NO:4) of the molecule and the protein encoded by such sequence has the same (i.e., within an order of magnitude) galactokinase activity as the protein encoded by SEQ ID NO:4. As used herein, substantially similar refers to the sequences having similar identity to the sequences of the instant invention. Thus
25 nucleotide sequences that are substantially the same can be identified by hybridization or by sequence comparison. Protein sequences that are substantially the same can be identified by one or more of the following: proteolytic digestion, gel electrophoresis and/or microsequencing.

This invention also provides isolated nucleic acid molecules encoding a missense mutation (SEQ ID NO:5) or a nonsense mutation (SEQ ID NO:6) of the
30 human galactokinase protein and DNA sequences which are degenerate to SEQ ID NO:5 or 6. Degenerate DNA sequences encode the same amino acid (or termination site) sequence as SEQ ID NO:5 or 6, but have variation(s) in the nucleotide coding sequences.

35 One means for isolating a nucleic acid molecule encoding for a human galactokinase is to probe a human genomic or cDNA library with a natural or artificially designed probe using art recognized procedures (See for example: "Current Protocols in Molecular Biology", Ausubel, F.M., et al. (eds.) Greene Publishing Assoc. and John Wiley Interscience, New York, 1989,1992). It is
40 appreciated to one skilled in the art that SEQ ID NO:4, or fragments thereof (comprising at least 15 contiguous nucleotides), is a particularly useful probe.

5 Several particularly useful probes for this purpose are set forth in Table 1, or hybridizable fragments thereof (i.e., comprising at least 15 contiguous nucleotides). It is also appreciated that such probes can be and are preferably labeled with an analytically detectable reagent to facilitate identification of the probe. Useful reagents include but are not limited to radioactivity, fluorescent dyes or enzymes
10 capable of catalyzing the formation of a detectable product. The probes are thus useful to isolate complementary copies of genomic DNA, cDNA or RNA from human, mammalian or other animal sources or to screen such sources for related sequences (e.g., additional members of the family, type and/or subtype) and including transcriptional regulatory and control elements defined above as well as
15 other stability, processing, translation and tissue specificity-determining regions from 5' and/or 3' regions relative to the coding sequences disclosed herein.

This invention also provides for gene therapy. "Gene therapy" means gene supplementation. That is, an additional (i.e., reference) copy of the gene of interest is inserted into a patients' cells. As a result, the protein encoded by the reference
20 gene corrects the defect (i.e., galactokinase deficiency) and permits the cells to function normally thus alleviating disease symptoms.

Gene therapy of the present invention can occur *in vivo* or *ex vivo*. *Ex vivo* gene therapy requires the isolation and purification of patient cells, the introduction of a therapeutic gene, and introduction of the genetically altered cells back into the
25 patient. A replication-deficient virus such as a modified retrovirus can be used to introduce the therapeutic gene (galactokinase) into such cells. For example, mouse Moloney leukemia virus (MMLV) is a well-known vector in clinical gene therapy trials (see, e.g., Boris-Lauerie et al., *Curr. Opin. Genet. Dev.*, 3:102-109 (1993)).

In contrast, *in vivo* gene therapy does not require isolation and purification
30 of patients' cells. The therapeutic gene is typically "packaged" for administration to a patient such as in liposomes or in a replication-deficient virus such as adenovirus (see, e.g., Berkner, K.L., *Curr. Top. Microbiol. Immunol.*, 158:39-66 (1992)) or adeno-associated virus (AAV) vectors (see, e.g., Muzyczka, N., *Curr. Top. Microbiol. Immunol.*, 158:97-129 (1992) and U.S. Patent 5,252,479 "Safe Vector
35 for Gene Therapy"). Another approach is administration of so-called "naked DNA" in which the therapeutic gene is directly injected into the bloodstream or muscle tissue.

Cell types useful for gene therapy of the present invention include
40 hepatocytes, fibroblasts, lymphocytes, any cell of the eye (e.g., retina), epithelial and endothelial cells. Preferably the cells are hepatocytes, any cell of the eye or respiratory (or pulmonary) epithelial cells. Transfection of (pulmonary) epithelial

5 cells can occur via inhalation of a nebulized preparation of DNA vectors in liposomes, DNA-protein complexes or replication-deficient adenoviruses (see, e.g., U.S. Patent 5,240,846 "Gene Therapy Vector for Cystic Fibrosis".

This invention also provides for a process to prepare human galactokinase proteins. Non-mutant proteins are defined with reference to the amino acid sequence listed in SEQ ID NO:4 and includes variants with a substantially similar amino acid sequence that have the same galactokinase activity. Additional proteins of this invention include mutant human galactokinase proteins as set forth in SEQ ID NO: 5 or 6. The proteins of this invention are preferably made by recombinant genetic engineering techniques. The isolated nucleic acids particularly the DNAs can be introduced into expression vectors by operatively linking the DNA to the necessary expression control regions (e.g., regulatory regions) required for gene expression. The vectors can be introduced into the appropriate host cells such as prokaryotic (e.g., bacterial), or eukaryotic (e.g., yeast or mammalian) cells by methods well known in the art (Ausubel et al., *supra*). The coding sequences for the desired 10 proteins having been prepared or isolated, can be cloned into any suitable vector or replicon. Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. Examples of recombinant DNA vectors for cloning and host cells which they can transform include, but is not limited to, the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5 (*Saccharomyces*), a baculovirus insect cell system, a *Drosophila* insect system, and YCp19 (*Saccharomyces*). See, generally, 15 "DNA Cloning": Vols. I & II, Glover et al. ed. IRL Press Oxford (1985) (1987) and; T. Maniatis et al. ("Molecular Cloning" Cold Spring Harbor Laboratory (1982). 20

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the 25 desired protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The subunit antigens of the present invention can be expressed using, for example, the *E. coli* tac promoter or the protein A gene (spa) promoter and signal sequence. Leader sequences can be removed by the 30 bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 4,425,437; 4,338,397.

5 In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence
10 of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control
15 sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the sequences encoding the particular antigen of interest may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be
20 attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an
25 appropriate restriction site.

In some cases, it may be desirable to produce other mutants or analogs of the galactokinase protein. Mutants or analogs may be prepared by the deletion of a portion of the sequence encoding the protein, by insertion of a sequence, and/or by substitution of one or more nucleotides within the sequence. Techniques for
30 modifying nucleotide sequences, such as site-directed mutagenesis, are well known to those skilled in the art. See, e.g., T. Maniatis et al., *supra*; DNA Cloning, Vols. I and II, *supra*; Nucleic Acid Hybridization, *supra*.

A number of prokaryotic expression vectors are known in the art.
See, e.g., U.S. Patent Nos. 4,578,355; 4,440,859; 4,436,815; 4,431,740; 4,431,739;
35 4,428,941; 4,425,437; 4,418,149; 4,411,994; 4,366,246; 4,342,832; see also U.K.
Patent Applications GB 2,121,054; GB 2,008,123; GB 2,007,675; and European
Patent Application 103,395. Yeast expression vectors are also known in the art. See,
e.g., U.S. Patent Nos. 4,446,235; 4,443,539; 4,430,428; see also European Patent
Applications 103,409; 100,561; 96,491. pSV2neo (as described in J. Mol. Appl.
40 Genet. 1:327-341) which uses the SV40 late promoter to drive expression in
mammalian cells or pCDNA1neo, a vector derived from pCDNA1 (Mol. Cell Biol.

5 7:4125-29) which uses the CMV promoter to drive expression. Both these latter two vectors can be employed for transient or stable (using G418 resistance) expression in mammalian cells. Insect cell expression systems, e.g., *Drosophila*, are also useful, see for example, PCT applications WO 90/06358 and WO 92/06212 as well as EP 290,261-B1.

10 Depending on the expression system and host selected, the proteins of the present invention are produced by growing host cells transformed by an expression vector described above under conditions whereby the protein of interest is expressed. Preferred mammalian cells include human embryonic kidney cells, monkey kidney (HEK-293cells), fibroblast (COS) cells, Chinese hamster ovary (CHO) cells, 15 *Drosophila* or murine L-cells. If the expression system secretes the protein into growth media, the protein can be purified directly from the media. If the protein is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

20 An alternative method to identify proteins of the present invention is by constructing gene libraries, using the resulting clones to transform *E. coli* and pooling and screening individual colonies using polyclonal serum or monoclonal antibodies to galactokinase.

25 The proteins of the present invention may also be produced by chemical synthesis such as solid phase peptide synthesis, using known amino acid sequences or amino acid sequences derived from the DNA sequence of the genes of interest. Such methods are known to those skilled in the art. Chemical synthesis of peptides is not particularly preferred.

30 The proteins of the present invention or their fragments comprising at least one epitope can be used to produce antibodies, both polyclonal and monoclonal. If polyclonal antibodies are desired, a selected mammal, (e.g., mouse, rabbit, goat, horse, etc.) is immunized with the protein of the present invention, or a fragment thereof, capable of eliciting an immune response (i.e., having at least one epitope). Serum from the immunized animal is collected and treated according to known 35 procedures. If serum containing polyclonal antibodies is used, the polyclonal antibodies can be purified by immunoaffinity chromatography or other known procedures.

40 Monoclonal antibodies to the proteins of the present invention, and to the fragments thereof, can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by using hybridoma technology is well known. Immortal antibody-producing cell lines can be created by

- 5 cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., M. Schreier et al., "Hybridoma Techniques" (1980); Hammerling et al., "Monoclonal Antibodies and T-cell Hybridomas" (1981); Kennett et al., "Monoclonal Antibodies" (1980); see also U.S. Patent Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,452,570; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against the antigen of interest, or fragment thereof, can be screened for various properties; i.e., for isotype, epitope, affinity, etc. Hence one skilled in the art can produce monoclonal antibodies specifically reactive with mutant galactokinase proteins, e.g., the missense mutation of SEQ ID NO:5 or nonsense mutation of SEQ ID NO:6. Monoclonal antibodies are useful in purification, using immunoaffinity techniques, of the individual antigens which they are directed against. Alternatively, genes encoding the monoclonals of interest may be isolated from the hybridomas by PCR techniques known in the art and cloned and expressed in the appropriate vectors. The antibodies of this invention, whether polyclonal or monoclonal have additional utility in that they may be employed reagents in immunoassays, RIA, ELISA, and the like. As used herein, "monoclonal antibody" is understood to include antibodies derived from one species (e.g., murine, rabbit, goat, rat, human, etc.) as well as antibodies derived from two (or perhaps more) species (e.g., chimeric and humanized antibodies).
- 25 Chimeric antibodies, in which non-human variable regions are joined or fused to human constant regions (see, e.g. Liu et al., Proc. Natl Acad. Sci. USA, 84:3439 (1987)), may also be used in assays or therapeutically. Preferably, a therapeutic monoclonal antibody would be "humanized" as described in Jones et al., Nature, 321:522 (1986); Verhoeyen et al.; Science, 239:1534 (1988); Kabat et al., J. Immunol., 147:1709 (1991); Queen et al., Proc. Natl Acad. Sci. USA, 86:10029 (1989); Gorman et al., Proc. Natl Acad. Sci. USA, 88:34181 (1991); and Hodgson et al., Bio/Technology, 9:421 (1991). Therefore, this invention also contemplates antibodies, polyclonal or monoclonal (including chimeric and "humanized") directed to epitopes corresponding to amino acid sequences disclosed herein from human galactokinase. Methods for the production of polyclonal and monoclonal antibodies are well known, see for example Chap. 11 of Ausubel et al. (supra).
- 30 When the antibody is labeled with an analytically detectable reagent such as radioactivity, fluorescence, or an enzyme, the antibody can be used to detect the presence or absence of human galactokinase and/or its quantitative level. In addition, 40 antibodies (polyclonal or monoclonal) specific for the missense and nonsense mutations of the present invention are useful for diagnostic purposes. A serum or

- 5 tissue sample (e.g., liver, lung, etc.) is obtained and allowed to come in contact with an antibody or antibody fragment which specifically binds to a mutant human galactokinase protein of the invention under conditions such that an antigen-antibody complex is formed between said antibody (or antibody fragment) and said mutant galactokinase protein. The detection for the presence or absence of said
10 complex is within the skill of the art (e.g., ELISA, RIA, Western Blotting, Optical Biosensor (e.g., BIACore - Pharmacia Biosensor, Uppsala, Sweden) and do not limit this invention.

This invention also contemplates pharmaceutical compositions comprising an effective amount of the galactokinase protein of the invention and a
15 pharmaceutically acceptable carrier. Pharmaceutical compositions of proteinaceous drugs of this invention are particularly useful for parenteral administration, i.e., subcutaneously, intramuscularly or intravenously. Optionally, the galactokinase protein is surrounded by a membrane bound vesicle, such as a liposome.

The compositions for parenteral administration will commonly comprise a
20 solution of the compounds of the invention or a cocktail thereof dissolved in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be employed, e.g., water, buffered water, 0.4% saline, 0.3% glycine, and the like. These solutions are sterile and generally free of particulate matter. These solutions may be sterilized by conventional, well known sterilization techniques. The
25 compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, etc. The concentration of the compound of the invention in such pharmaceutical formulation can very widely, i.e., from less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be selected
30 primarily based on fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain 1 mL sterile buffered water, and 50 mg of a compound of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain 250 ml of sterile Ringer's solution, and 150 mg of a compound of the invention. Actual methods for preparing parenterally administrable compositions are well known or will be apparent to those skilled in the art and are described in more detail in, for example, Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pennsylvania.

40 The compounds described herein can be lyophilized for storage and reconstituted in a suitable carrier prior to use. This technique has been shown to be

5 effective with conventional proteins and art-known lyophilization and reconstitution techniques can be employed.

The physician will determine the dosage of the present therapeutic agents which will be most suitable and it will vary with the form of administration and the particular compound chosen, and furthermore, it will vary with the particular patient
10 under patient under treatment. He will generally wish to initiate treatment with small dosages substantially less than the optimum dose of the compound and increase the dosage by small increments until the optimum effect under the circumstances is reached. It will generally be found that when the composition is administered orally, larger quantities of the active agent will be required to produce the same effect as a
15 smaller quantity given parenterally. The therapeutic dosage will generally be from 1 to 10 milligrams per day and higher although it may be administered in several different dosage units.

Depending on the patient condition, the pharmaceutical composition of the invention can be administered for prophylactic and/or therapeutic treatments. In
20 therapeutic application, compositions are administered to a patient already suffering from a disease in an amount sufficient to cure or at least partially arrest the disease and its complications. In prophylactic applications, compositions containing the present compounds or a cocktail thereof are administered to a patient not already in a disease state to enhance the patient's resistance.

25 Single or multiple administrations of the pharmaceutical compositions can be carried out with dose levels and pattern being selected by the treating physician. In any event, the pharmaceutical composition of the invention should provide a quantity of the compounds of the invention sufficient to effectively treat the patient.

This invention also contemplates use of the galactokinase genes of the instant
30 invention as a diagnostic. For example, some diseases result from inherited defective genes. These genes can be detected by comparing the sequence of the defective gene with that of a normal one. Subsequently, one can verify that a "mutant" gene is associated with galactokinase deficiency by measurement of galactose. That is, a mutant gene would be associated with (atypically) elevated
35 levels of galactose in a patient. In addition, one can insert mutant galactokinase genes into a suitable vector for expression in a functional assay system (e.g., colorimetric assay, expression on MacConkey plates, complementation experiments, e.g, in a galactokinase deficient strain of yeast or *E. coli*) as yet another means to verify or identify galactokinase mutations. As an example, RNA from an individual
40 can be transcribed with reverse transcriptase to cDNA which can then be amplified by polymerase chain reaction (PCR), cloned into an *E. coli* expression vector, and

5 transformed into a galactokinase-deficient strain of *E. coli*. When grown on MacConkey indicator plates, galactokinase-deficient cells will produce colonies that are white in color, whereas cells that have been transformed/complemented with a functional galactokinase gene will be red (see, e.g., Examples section). If most to all of the colonies from an individual are red, then the individual is considered to be
10 normal with respect to galactokinase activity. If approximately 50% of the colonies are red (the other 50% white), then that individual is likely to be a carrier for galactokinase deficiency. If most to all of the colonies are white, then that individual is likely to be galactokinase deficient. Once "mutant" genes have been identified, one can then screen the population for carriers of the "mutant"
15 galactokinase gene. (A carrier is a person in apparent health whose chromosomes contain a "mutant" galactokinase gene that may be transmitted to that person's offspring.) In addition, monoclonal antibodies that are specific for the mutant galactokinase proteins can be used for diagnostic purposes as described above.

Individuals carrying mutations in the human galactokinase gene may be
20 detected at the DNA level by a variety of techniques. Nucleic acids used for diagnosis (genomic DNA, mRNA, etc.) may be obtained from a patient's cells, such as from blood, urine, saliva, tissue biopsy (e.g., chorionic villi sampling or removal of amniotic fluid cells), and autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR, ligase chain reaction (LCR), strand displacement amplification (SDA), etc. (see, e.g., Saiki et al., *Nature*, 324:163-166 (1986), Bej, et al., *Crit. Rev. Biochem. Molec. Biol.*, 26:301-334 (1991), Birkenmeyer et al., *J. Virol. Meth.*, 35:117-126 (1991), Van Brunt, J., *Bio/Technology*, 8:291-294 (1990)) prior to analysis. RNA may also be used for the same purpose. The RNA can be reverse-transcribed and amplified at one time
25 with PCR-RT (polymerase chain reaction - reverse transcriptase) or reverse-transcribed to an unamplified cDNA. As an example, PCR primers complementary to the nucleic acid of the instant invention can be used to identify and analyze galactokinase mutations. For example, deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal galactokinase
30 genotype. Point mutations can be identified by hybridizing amplified DNA to radiolabeled galactokinase RNA (of the invention) or alternatively, radiolabelled galactokinase antisense DNA sequences (of the invention). Perfectly matched sequences can be distinguished from mismatched duplexes by RNase A digestion or by differences in melting temperatures (T_m). Such a diagnostic would be particularly
35 useful for prenatal and even neonatal testing.

5 In addition, point mutations and other sequence differences between the reference gene and "mutant" genes can be identified by yet other well-known techniques, e.g., direct DNA sequencing, single-strand conformational polymorphism (SSCP; Orita et al., *Genomics*, 5:874-879 (1989)). For example, a sequencing primer is used with double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed by conventional procedures with radiolabeled nucleotides or by automatic sequencing procedures with fluorescent-tags. Cloned DNA segments may also be used as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. The presence of nucleotide repeats may correlate to a change in galactokinase activity (causative change) or serve as marker for various polymorphisms.

10 Genetic testing based on DNA sequence differences may be achieved by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized by high resolution gel electrophoresis. DNA fragments of different sequences may be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (see, e.g., Myers et al., *Science*, 230:1242 (1985)). In addition, sequence alterations, in particular small deletions, may be detected as changes in the migration pattern of DNA heteroduplexes in non-denaturing gel electrophoresis (i.e., heteroduplex electrophoresis) (see, e.g., Nagamine et al., *Am. J. Hum. Genet.*, 45:337-339 (1989)).

15 Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (e.g., Cotton et al., *Proc. Natl. Acad. Sci. USA*, 85:4397-4401 (1985)).

20 Thus, the detection of a specific DNA sequence may be achieved by methods such as hybridization (e.g., heteroduplex electroporation, see, White et al., *Genomics*, 12:301-306 (1992)), RNase protection (e.g., Myers et al., *Science*, 230:1242 (1985)) chemical cleavage (e.g., Cotton et al., *Proc. Natl. Acad. Sci. USA*, 85:4397-4401 (1985))), direct DNA sequencing, or the use of restriction enzymes (e.g., restriction fragment length polymorphisms (RFLP) in which variations in the number and size of restriction fragments can indicate insertions, deletions, presence of nucleotide repeats and any other mutation which creates or destroys an endonuclease restriction sequence). Southern blotting of genomic DNA may also be used to identify large (i.e., greater than 100 base pair) deletions and insertions.

5 In addition to more conventional gel-electrophoresis, and DNA sequencing, mutations (e.g., microdeletions, aneuploidies, translocations, inversions) can also be detected by *in situ* analysis (See, e.g., Keller et al., DNA Probes, 2nd Ed., Stockton Press, New York, N.Y., USA (1993)). That is, DNA (or RNA) sequences in cells can be analyzed for mutations without isolation and/or immobilization onto a
10 membrane. Fluorescence *in situ* hybridization (FISH) is presently the most commonly applied method and numerous reviews of FISH have appeared. See, e.g., Trachuck et al., Science, 250:559-562 (1990), and Trask et al., Trends Genet., 7: 149-154 (1991) which are incorporated herein by reference for background purposes. Hence, by using nucleic acids based on the structure of specific genes,
15 e.g., galactokinase, one can develop diagnostic tests for galactokinase deficiency.

In addition, some diseases are a result of, or are characterized by, changes in gene expression which can be detected by changes in the mRNA. Alternatively, the galactokinase gene can be used as a reference to identify individuals expressing a decreased level of galactokinase, e.g., by Northern blotting or *in situ* hybridization.

20 Defining appropriate hybridization conditions is within the skill of the art. See, e.g., "Current Protocols in Mol. Biol." Vol. I & II, Wiley Interscience. Ausbel et al. (ed.) (1992). Probing technology is well known in the art and it is appreciated that the size of the probes can vary widely but it is preferred that the probe be at least 15 nucleotides in length. It is also appreciated that such probes can be and are
25 preferably labeled with an analytically detectable reagent to facilitate identification of the probe. Useful reagents include but are not limited to radioactivity, fluorescent dyes or enzymes capable of catalyzing the formation of a detectable product. As a general rule the more stringent the hybridization conditions the more closely related genes will be that are recovered.

30 Also within the scope of this invention are antisense oligonucleotides predicated upon the sequences disclosed herein for human galactokinase. Synthetic oligonucleotides or related antisense chemical structural analogs are designed to recognize and specifically bind to a target nucleic acid encoding galactokinase and galactokinase mutations. The general field of antisense technology is illustrated by
35 the following disclosures which are incorporated herein by reference for purposes of background (Cohen, J.S., Trends in Pharm. Sci., 10:435(1989) and Weintraub, H.M. Scientific American, Jan.(1990) at page 40).

40 Transgenic, non-human, animals may be obtained by transfecting appropriate fertilized eggs or embryos of a host with nucleic acids encoding human galactokinase disclosed herein, see for example U.S. Patents 4,736,866; 5,175,385; 5,175,384 and 5,175,386. The resultant transgenic animal may be used as a model for the study of

- 5 galactokinase. Particularly, useful transgenic animals are those which display a detectable phenotype associated with the expression of the receptor. Drugs may then be screened for their ability to reverse or exacerbate the relevant phenotype. This invention also contemplates operatively linking the receptor coding gene to regulatory elements which are differentially responsive to various temperature or
10 metabolic conditions, thereby effectively turning on or off the phenotypic expression in response to those conditions.

Although not necessarily limiting of this invention, following are some experimental data illustrative of this invention.

15

EXAMPLE I

Purification of Human Galactokinase from Placental Tissue

Galactokinase (galK) was obtained from human placenta as described by Stambolian et al. (*Biochim Biophys Acta*, 831:306-312 (1985)), which is incorporated by reference in its entirety. In essence, human placenta tissue (obtained within 1 hour of parturition) was homogenized, centrifuged and the resulting supernatant was absorbed onto DEAE-Sephadex®. The material was eluted, precipitated with ammonium sulfate and then run through a sizing column (Sephadex G-100 SF®). Pooled active fractions were concentrated. Purified protein was obtained following separation by SDS polyacrylamide electrophoresis and then Western blotted using standard techniques (see, Laemmli, *Nature*, 227:680-685 (1970), or LeGendre et al., *Biotechniques*, 6:154 (1988)). Minute amounts of galactokinase were isolated (micrograms) from multiple rounds of protein purification. After a trypsin peptide digest, 7 peptide sequences were eventually isolated and identified. The three longest fragments are presented below:

[SEQ ID NO:1]

Val Asn Leu Ile Gly Glu His Thr Asp Tyr Asn Gln Gly Leu Val Leu-
Pro Met Ala Leu Glu Leu Met Thr Val Leu Val Gly Ser Pro Arg

35

[SEQ ID NO:2]

His Ile Gln Glu His Tyr Gly Gly Thr Ala Thr Phe Tyr Leu Ser Gln-
Ala Ala Asp Gly Ala Lys

40

[SEQ ID NO:3]

Ala Gln Val Cys Gln Gln Ala Glu His Ser Phe Ala Gly Met Pro Cys-
Gly Ile Met Asp Gln Phe Ile Ser Leu Met Gly Gln Lys

5 The fragments were compared with peptide sequences encoded by cDNAs, in which the cDNAs were partially sequenced. The cDNAs (also known as expressed sequence tags or ESTs) were obtained from Human Genome Sciences, Inc. (Rockville, MD, USA). The best alignments occurred with an EST sequence from a human osteoclastoma stromal cell library (SEQ ID NO:1 showed 100% identity over 10 18 contiguous amino acids) and an EST sequence from a human pituitary library (SEQ ID NO:2 showed 95.5% identity over 22 contiguous amino acids). A full-length cDNA from the human osteoclastoma stromal cell library was identified and sequenced (SEQ ID NO:4) in its entirety on an automated ABI 373A Sequencer. Sequencing was confirmed on both strands. The corresponding amino acid sequence 15 (SEQ ID NO:4) was compared against the peptide fragments identified above. SEQ ID NO:1 corresponds to amino acids 38-68 of the full-length human galactokinase protein. Similarly, SEQ ID NOs: 2 and 3 correspond to amino acids 367-388 and 167-195, respectively, of human galactokinase.

20 Analysis of the Human Galactokinase Gene:

A comparison of the amino acid sequence for human galactokinase with that of *E. coli* galactokinase (Debouck et al., Nuc. Acid Res., **13**:1841-1853 (1985)) shows 61% similarity and 44.5% identity. Further comparison with another purported human galactokinase gene (*GK2*) (Lee et al., Proc. Natl. Acad. Sci. USA, **89**:10887-25 10891 (1992)) shows 54% similarity and 34.6% identity at the amino acid level. Furthermore, the *GK2* gene maps to human chromosome 15 which is in contrast to the gene of the present invention which maps to human chromosome 17, position q24 as determined by fluorescence *in situ* hybridization (FISH) analysis.

SEQ ID NO:4 was hybridized against a Northern blot containing human messenger RNA from placenta, brain, skeletal muscle, kidney, intestine, heart, lung and liver according to standard procedures (see, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, 1989). Hybridization was strongest with human liver and lung tissue.

35 Galactokinase Complementation:

SEQ ID NO:4 was subcloned into an *E. coli* vector, plasmid pBluescript [Stratagene]. When transformed into C600K-, a galactokinase-deficient strain, the transformed *E. coli* grew on MacConkey agar plates containing 1% galactose (and ampicillin @ 50ug/ml for plasmid selection), and produced brick red colonies, indicating sugar fermentation. Specifically, the red color is due to the action of acids,

40

- 5 produced by galactose fermentation, upon bile salts and the indicator (neutral red) in MacConkey medium.

Expression in Mammalian Cells:

SEQ ID NO:4 was also subcloned into COS-1 cells [ATCC CRL 1650]. The
10 cells were transfected, grown, and cell lysates were prepared. The lysates were
assayed by a ^{14}C galactokinase assay as described by Stambolian et al. (*Exp. Eye Res.*,
38:231-237 (1984)) which is hereby incorporated by reference in its entirety. When
expressed in transiently transfected COS cells, galactokinase activity was tenfold
higher than control levels (6600 vs. 640 counts per minute - repeated three times).
15 These results definitively confirm that SEQ ID NO:4 encodes a full-length,
biologically active, human galactokinase gene.

The nucleic acid molecule of the invention can also be subcloned into an
expression vector to produce high levels of human galactokinase (either fused to
another protein, e.g., operatively linked at the 5' end with another coding sequence, or
20 unfused) in transfected cells. For mammalian cells, the expression vector would
optionally encode a neomycin resistance gene to select for transfectants on the basis of
ability to grow in G418 and a dihydrofolate reductase gene which permits
amplification of the transfected gene in DHFR⁻ cells. The plasmid can then be
introduced into host cell lines e.g., CHO ACC98, a nonadherent, DHFR⁻ cell line
25 adapted to grow in serum free medium, and human embryonic kidney 293 cells
(ATCC CRL 1573), and transfected cell lines can be selected by G418 resistance.

Human Galactokinase Gene - Genomic Sequence:

A full-length galactokinase genomic gene coding region was identified from a
30 lambda phage (λ Fix II) human genomic library (made from human placenta tissue)
using the galK cDNA as a probe. One isolate, designated clone 17 was deposited on
3 May 1995, with the American Type Culture Collection (ATCC), Rockville, MD,
USA, under accession number ATCC 97135, and has been accepted as a patent
deposit, in accordance with the Budapest Treaty of 1977 governing the deposit of
35 microorganisms for the purposes of patent procedure.

The genomic gene coding region is divided into at least 8 exons isolated from
4 DNA fragments. The arrangement is depicted in Figure 1. The DNA sequence was
determined by using multiple oligonucleotide PCR primers corresponding to the galK
cDNA sequence (i.e., corresponding to galK genomic exons) as well as
40 oligonucleotide PCR primers subsequently designed that correspond to non-coding
regions (i.e., galK genomic introns). Thus the structure of the galactokinase genomic
gene is summarized in Table 1 below (see also Figure 2 and SEQ ID NO:7]):

Table 1
Genomic Galactokinase Gene

| Exon # | Amino Acids Encoded | PCR Primer #/[SEQ ID NO] |
|--------|---------------------|--|
| 1 | 1-55 | 3333/[8] 3334/[9] 3598/[10] 3599/[11] |
| 2 | 56-118 | 1888/[12] 3332/[13] 3604/[14] 3605/[15] |
| 3 | 119-158 | 3331/[16] 3606/[17] |
| 4 | 159-204 | 1657/[18] 3034/[19] |
| 5 | 205-264 | 3330/[20] 3607/[21] |
| 6 | 265-315 | 1539/[22] 2665/[23] |
| 7 | 316-369 | 1891/[24] 2665/[25] |
| 8 | 370-392 | 2665/[26] 2666/[27] 2667/[28] |

10

Galactokinase Deficiency Marker/Gene:

15 A fibroblast cell line (GM00334), derived from a patient with galactokinase deficiency, was obtained from the Coriell Institute for Medical research, 401 Haddon

5 Ave., Camden, New Jersey, 08103. Total RNA was isolated from the cultured cells using the RAZOL kit for isolation of RNA (Biotecx, Houston, Tx). Cytoplasmic DNA (1 ug) was reversed transcribed with oligonucleotide primers 1823 [SEQ ID NO: 29] and 1825 [SEQ ID NO: 30]. The sample was amplified by 35 cycles at 94°C for 1 min., 60°C for 1 min. and 72°C for 7 min. The DNA product was purified 10 electrophoretically, ligated to the TA cloning vector (Invitrogen) and sequenced. Twelve cDNAs in total were sequenced (representing cloned PCR products of multiple independent PCR reactions). This procedure was also repeated with cultured fibroblasts from normal controls (i.e., persons not exhibiting galactokinase deficiency).

A comparison with normal controls identified a single base substitution of A 15 for G at position 122 of the "normal" human galactokinase gene [SEQ ID NO: 4]. The result is a missense mutation in amino acid 32 from Val to Met [SEQ ID NO: 5]. The G to A base change creates a MscI endonuclease restriction site (i.e., TGG↓CCA) on the mutant allele. This restriction site was then used to rapidly screen 20 for the mutant allele in the parents of the patient with galactokinase deficiency. In essence, the exon encoding galactokinase residues 1 to 5 (i.e., exon 1, see Table 1) was cloned from a genomic lambda phage library and its DNA sequence was determined, including a portion of the flanking intron sequences. Oligonucleotide primers (X2-5OUT [SEQ ID NO: 31] and X2-3OUT [SEQ ID NO: 32]) were 25 designed to hybridize to intron sequences for the amplification of a 346 bp DNA fragment of the genomic DNA. The PCR product was analyzed for the point mutation via RFLP, that is, the presence of a newly created MscI site as detected by electrophoresis of a 1.5% agarose gel. A "normal" allele remains uncut with the enzyme MscI, and thus migrates as a 346bp fragment on an agarose gel. The PCR product from the patient with galactokinase deficiency (i.e., the G to A base change) is 30 cleaved with MscI, resulting in two fragments of 193 and 153 bp, respectively. The absence of 346 bp fragment indicates that the patient was homozygous for this allele. In contrast, PCR products from the parents of this patient, followed by a MscI digestion, resulted in three fragments (346, 193 and 153 bp) which is consistent with a 35 heterozygous pattern for the G to A base change. That is, the parents were both carriers of the same mutation.

To determine whether the missense mutation resulted in decreased enzymatic activity, a cDNA clone containing the G to A base change was subcloned into COS cells and assayed for galactokinase activity as previously described. COS cells transfected with cDNA encoding the missense mutation had the same level of 40 galactokinase activity as the host COS cells, namely 0.02 units/ug protein. In contrast, COS cells transfected with the non-mutant galactokinase cDNA [SEQ ID NO:4] had a

5 fifty-fold higher activity compared to the host COS cells (i.e., control). This results supports the Val³² to Met³² substitution as the cause of the decreased enzymatic activity.

Another mutation was discovered in an unrelated patient having cataracts and diagnosed as galactokinase deficient (galactokinase activity was found to be close to zero). Genomic DNA was isolated from lymphoblastoid cell lines and sequenced by 10 automated sequencing on an ABI 373A sequencer. A single base substitution of T for G resulted in an in-frame nonsense codon (i.e., TAG) at amino acid position 80 [SEQ ID NO:6]. This mutation causes premature termination of human galactokinase, resulting in a truncated protein of 79 amino acids that would be expected to be non-functional. (The genomic DNA of the parents of this patient were heterozygous for 15 this mutation, and hence not galactokinase deficient.)

The above description and examples fully disclose the invention including 20 preferred embodiments thereof. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments herein. Such equivalents are intended to be within the scope of the following claims.

5

SEQUENCE LISTING

(1) GENERAL INFORMATION:

10 (1) APPLICANT: Bergsma, Derk J.
Stambolian, Dwight

(ii) TITLE OF INVENTION: Human Galactokinase Gene

15 (iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: SmithKline Beecham Corp./Corporate
Intellectual Property
(B) STREET: 709 Swedeland Road/UW2220
(C) CITY: King of Prussia
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19406-0939

25 (v) COMPUTER READABLE FORM:

30 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

35 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: PCT/US94/10825
(B) FILING DATE: 23-SEP-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sutton, Jeffrey A.
(B) REGISTRATION NUMBER: 34,028
(C) REFERENCE/DOCKET NUMBER: P50268-1

5

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5024
- (B) TELEFAX: 610-270-5090

10

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Ile | Gly | Glu | His | Thr | Asp | Tyr | Asn | Gln | Gly | Leu | Val | Leu |
| 1 | | | | | | | | | | | | | | 10 | 15 |

30

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Pro | Met | Ala | Leu | Glu | Leu | Met | Thr | Val | Leu | Val | Gly | Ser | Pro | Arg | |
| | | | | | | | | | | | | | 20 | 25 | 30 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

His Ile Gln Glu His Tyr Gly Gly Thr Ala Thr Phe Tyr Leu Ser Gln
1 5 10 15

10 Ala Ala Asp Gly Ala Lys
20

(2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Gln Val Cys Gln Gln Ala Glu His Ser Phe Ala Gly Met Pro Cys
1 5 10 15

30 Gly Ile Met Asp Gln Phe Ile Ser Leu Met Gly Gln Lys
20 25

(2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 29..1204

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTGGCA CGAGTGCAGG CGCGCGTC ATG GCT GCT TTG AGA CAG CCC CAG
52 Met Ala Ala Leu Arg Gln Pro Gln
15 1 5

GTC GCG GAG CTG CTG GCC GAG GCC CGG CGA GCC TTC CGG GAG GTC
100 Val Ala Glu Leu Leu Ala Glu Ala Arg Arg Ala Phe Arg Glu Glu Phe
20 10 15 20

GGG GCC GAG CCC GAG CTG GCC GTG TCA GCG CCG GGC CGC GTC AAC CTC
148 Gly Ala Glu Pro Glu Leu Ala Val Ser Ala Pro Gly Arg Val Asn Leu
25 25 30 35 40

ATC GGG GAA CAC ACG GAC TAC AAC CAG GGC CTG GTG CTG CCT ATG GCT
196 Ile Gly Glu His Thr Asp Tyr Asn Gln Gly Leu Val Leu Pro Met Ala
30 45 50 55

CTG GAG CTC ATG ACG GTG CTG GTG GGC AGC CCC CGC AAG GAT GGG CTG
244 Leu Glu Leu Met Thr Val Leu Val Gly Ser Pro Arg Lys Asp Gly Leu
35 60 65 70

GTG TCT CTC CTC ACC ACC TCT GAG GGT GCC GAT GAG CCC CAG CGG CTG
292 Val Ser Leu Leu Thr Thr Ser Glu Gly Ala Asp Glu Pro Gln Arg Leu
40 75 80 85

CAG TTT CCA CTG CCC ACA GCC CAG CGC TCG CTG GAG CCT GGG ACT CCT
340 Gln Phe Pro Leu Pro Thr Ala Gln Arg Ser Leu Glu Pro Gly Thr Pro

| | | | |
|--|--|-----|-----|
| 5 | 90 | 95 | 100 |
| CGG TGG GCC AAC TAT GTC AAG GGA GTG ATT CAG TAC TAC CCA GCT GCC 388 | | | |
| 10 | Arg Trp Ala Asn Tyr Val Lys Gly Val Ile Gln Tyr Tyr Pro Ala Ala 105 | 110 | 115 |
| 120 | | | |
| CCC CTC CCT GGC TTC AGT GCA GTG GTG GTC AGC TCA GTG CCC CTG GGG 436 | | | |
| 15 | Pro Leu Pro Gly Phe Ser Ala Val Val Val Ser Ser Val Val Pro Leu Gly 125 | 130 | 135 |
| GGT GGC CTG TCC AGC TCA GCA TCC TTG GAA GTG GCC ACG TAC ACC TTC 484 | | | |
| 20 | Gly Gly Leu Ser Ser Ser Ala Ser Leu Glu Val Ala Thr Tyr Thr Phe 140 | 145 | 150 |
| CTC CAG CAG CTC TGT CCA GAC TCG GGC ACA ATA GCT GCC CGC GCC CAG 532 | | | |
| 25 | Leu Gln Gln Leu Cys Pro Asp Ser Gly Thr Ile Ala Ala Arg Ala Gln 155 | 160 | 165 |
| GTG TGT CAG CAG GCC GAG CAC AGC TTC GCA GGG ATG CCC TGT GGC ATC 580 | | | |
| 30 | Val Cys Gln Gln Ala Glu His Ser Phe Ala Gly Met Pro Cys Gly Ile 170 | 175 | 180 |
| ATG GAC CAG TTC ATC TCA CTT ATG GGA CAG AAA GGC CAC GCG CTG CTC 628 | | | |
| 35 | Met Asp Gln Phe Ile Ser Leu Met Gly Gln Lys Gly His Ala Leu Leu 185 | 190 | 195 |
| 200 | | | |
| ATT GAC TGC AGG TCC TTG GAG ACC AGC CTG GTG CCA CTC TCG GAC CCC 676 | | | |
| 40 | Ile Asp Cys Arg Ser Leu Glu Thr Ser Leu Val Pro Leu Ser Asp Pro 205 | 210 | 215 |
| AAG CTG GCC GTG CTC ATC ACC AAC TCT AAT GTC CGC CAC TCC CTG GCC 724 | | | |
| Lys Leu Ala Val Leu Ile Thr Asn Ser Asn Val Arg His Ser Leu Ala | | | |

| | | | |
|---|-----|-----|-----|
| 5 | 220 | 225 | 230 |
| TCC AGC GAG TAC CCT GTG CGG CGG CGC CAA TGT GAA GAA GTG GCC CGG 772 | | | |
| Ser Ser Glu Tyr Pro Val Arg Arg Arg Gln Cys Glu Glu Val Ala Arg | | | |
| 10 | 235 | 240 | 245 |
| GCG CTG GGC AAG GAA AGC CTC CGG GAG GTA CAA CTG GAA GAG CTA GAG 820 | | | |
| Ala Leu Gly Lys Glu Ser Leu Arg Glu Val Gln Leu Glu Leu Glu | | | |
| 15 | 250 | 255 | 260 |
| GCT GCC AGG GAC CTG GTG AGC AAA GAG GGC TTC CGG CGG GCC CGG CAC 868 | | | |
| Ala Ala Arg Asp Leu Val Ser Lys Glu Gly Phe Arg Arg Ala Arg His | | | |
| 20 | 265 | 270 | 275 |
| GTG GTG GGG GAG ATT CGG CGC ACG GCC CAG GCA GCG GCC GCC CTG AGA 916 | | | |
| Val Val Gly Glu Ile Arg Arg Thr Ala Gln Ala Ala Ala Leu Arg | | | |
| 25 | 285 | 290 | 295 |
| CGT GGC GAC TAC AGA GCC TTT GGC CGC CTC ATG GTG GAG AGC CAC CGC 964 | | | |
| Arg Gly Asp Tyr Arg Ala Phe Gly Arg Leu Met Val Glu Ser His Arg | | | |
| 30 | 300 | 305 | 310 |
| TCA CTC AGA GAC GAC TAT GAG GTG AGC TGC CCA GAG CTG GAC CAG CTG 1012 | | | |
| Ser Leu Arg Asp Asp Tyr Glu Val Ser Cys Pro Glu Leu Asp Gln Leu | | | |
| 35 | 315 | 320 | 325 |
| GTG GAG GCT GCG CTT GCT GTG CCT GGG GTT TAT GGC AGC CGC ATG ACG 1060 | | | |
| Val Glu Ala Ala Leu Ala Val Pro Gly Val Tyr Gly Ser Arg Met Thr | | | |
| 40 | 330 | 335 | 340 |
| GGC GGT GGC TTC GGT GGC TGC ACG GTG ACA CTG CTG GAG GCC TCC GCT 1108 | | | |
| Gly Gly Gly Phe Gly Gly Cys Thr Val Thr Leu Leu Glu Ala Ser Ala | | | |

(2) INFORMATION FOR SEQ ID NO:5:

40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 29..1204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTGGCA CGAGTGCAGG CGCGCGTC ATG GCT GCT TTG AGA CAG CCC CAG
52
Met Ala Ala Leu Arg Gln Pro Gln
10 1 5

GTC GCG GAG CTG CTG GCC GAG GCC CGG CGA GCC TTC CGG GAG GAG TTC
100
Val Ala Glu Leu Leu Ala Glu Ala Arg Arg Ala Phe Arg Glu Glu Phe
15 10 15 20

GGG GCC GAG CCC GAG CTG GCC ATG TCA GCG CCG GGC CGC GTC AAC CTC
148
Gly Ala Glu Pro Glu Leu Ala Met Ser Ala Pro Gly Arg Val Asn Leu
20 25 30 35 40

ATC GGG GAA CAC ACG GAC TAC AAC CAG GGC CTG GTG CTG CCT ATG GCT
196
Ile Gly Glu His Thr Asp Tyr Asn Gln Gly Leu Val Leu Pro Met Ala
25 45 50 55

CTG GAG CTC ATG ACG GTG CTG GTG GGC AGC CCC CGC AAG GAT GGG CTG
244
Leu Glu Leu Met Thr Val Leu Val Gly Ser Pro Arg Lys Asp Gly Leu
30 60 65 70

GTG TCT CTC CTC ACC ACC TCT GAG GGT GCC GAT GAG CCC CAG CGG CTG
292
Val Ser Leu Leu Thr Thr Ser Glu Gly Ala Asp Glu Pro Gln Arg Leu
35 75 80 85

CAG TTT CCA CTG CCC ACA GCC CAG CGC TCG CTG GAG CCT GGG ACT CCT
340
Gln Phe Pro Leu Pro Thr Ala Gln Arg Ser Leu Glu Pro Gly Thr Pro
40 90 95 100

CGG TGG GCC AAC TAT GTC AAG GGA GTG ATT CAG TAC TAC CCA GCT GCC
388
Arg Trp Ala Asn Tyr Val Lys Gly Val Ile Gln Tyr Tyr Pro Ala Ala

| | | | | |
|----|---|-----|-----|-----|
| 5 | 105 | 110 | 115 | 120 |
| | CCC CTC CCT GGC TTC AGT GCA GTG GTG GTC AGC TCA GTG CCC CTG GGG | | | |
| | 436 | | | |
| 10 | Pro Leu Pro Gly Phe Ser Ala Val Val Val Ser Ser Val Pro Leu Gly | | | |
| | 125 | 130 | 135 | |
| | GGT GGC CTG TCC AGC TCA GCA TCC TTG GAA GTG GCC ACG TAC ACC TTC | | | |
| | 484 | | | |
| 15 | Gly Gly Leu Ser Ser Ser Ala Ser Leu Glu Val Ala Thr Tyr Thr Phe | | | |
| | 140 | 145 | 150 | |
| | CTC CAG CAG CTC TGT CCA GAC TCG GGC ACA ATA GCT GCC CGC GCC CAG | | | |
| | 532 | | | |
| 20 | Leu Gln Gln Leu Cys Pro Asp Ser Gly Thr Ile Ala Ala Arg Ala Gln | | | |
| | 155 | 160 | 165 | |
| | GTG TGT CAG CAG GCC GAG CAC AGC TTC GCA GGG ATG CCC TGT GGC ATC | | | |
| | 580 | | | |
| 25 | Val Cys Gln Gln Ala Glu His Ser Phe Ala Gly Met Pro Cys Gly Ile | | | |
| | 170 | 175 | 180 | |
| | ATG GAC CAG TTC ATC TCA CTT ATG GGA CAG AAA GGC CAC GCG CTG CTC | | | |
| | 628 | | | |
| 30 | Met Asp Gln Phe Ile Ser Leu Met Gly Gln Lys Gly His Ala Leu Leu | | | |
| | 185 | 190 | 195 | 200 |
| | ATT GAC TGC AGG TCC TTG GAG ACC AGC CTG GTG CCA CTC TCG GAC CCC | | | |
| | 676 | | | |
| 35 | Ile Asp Cys Arg Ser Leu Glu Thr Ser Leu Val Pro Leu Ser Asp Pro | | | |
| | 205 | 210 | 215 | |
| | AAG CTG GCC GTG CTC ATC ACC AAC TCT AAT GTC CGC CAC TCC CTG GCC | | | |
| | 724 | | | |
| 40 | Lys Leu Ala Val Leu Ile Thr Asn Ser Asn Val Arg His Ser Leu Ala | | | |
| | 220 | 225 | 230 | |
| | TCC AGC GAG TAC CCT GTG CGG CGG CGC CAA TGT GAA GAA GTG GCC CGG | | | |
| | 772 | | | |
| | Ser Ser Glu Tyr Pro Val Arg Arg Arg Gln Cys Glu Glu Val Ala Arg | | | |

5 235 240 245

GCG CTG GGC AAG GAA AGC CTC CGG GAG GTA CAA CTG GAA GAG CTA GAG
820
Ala Leu Gly Lys Glu Ser Leu Arg Glu Val Gln Leu Glu Glu Leu Glu
10 250 255 260

GCT GCC AGG GAC CTG GTG AGC AAA GAG GGC TTC CGG CGG GCC CGG CAC
868
Ala Ala Arg Asp Leu Val Ser Lys Glu Gly Phe Arg Arg Ala Arg His
15 265 270 275 280

G TG GTG GGG GAG ATT CGG CGC ACG GCC CAG GCA GCG GCC GCC CTG AGA
916
Val Val Gly Glu Ile Arg Arg Thr Ala Gln Ala Ala Ala Ala Leu Arg
20 285 290 295

CGT GGC GAC TAC AGA GCC TTT GGC CGC CTC ATG GTG GAG AGC CAC CGC
964
Arg Gly Asp Tyr Arg Ala Phe Gly Arg Leu Met Val Glu Ser His Arg
25 300 305 310

TCA CTC AGA GAC GAC TAT GAG GTG AGC TGC CCA GAG CTG GAC CAG CTG
1012
Ser Leu Arg Asp Asp Tyr Glu Val Ser Cys Pro Glu Leu Asp Gln Leu
30 315 320 325

G TG GAG GCT GCG CTT GCT GTG CCT GGG GTT TAT GGC AGC CGC ATG ACG
1060
Val Glu Ala Ala Leu Ala Val Pro Gly Val Tyr Gly Ser Arg Met Thr
35 330 335 340

GGC GGT GGC TTC GGT GGC TGC ACG GTG ACA CTG CTG GAG GCC TCC GCT
1108
Gly Gly Gly Phe Gly Cys Thr Val Thr Leu Leu Glu Ala Ser Ala
40 345 350 355 360

GCT CCC CAC GCC ATG CGG CAC ATC CAG GAG CAC TAC GGC GGG ACT GCC
1156
Ala Pro His Ala Met Arg His Ile Gln Glu His Tyr Gly Thr Ala

5 365 370 375

ACC TTC TAC CTC TCT CAA GCA GCC GAT GGA GCC AAG GTG CTG TGC TTG
1204

Thr Phe Tyr Leu Ser Gln Ala Ala Asp Gly Ala Lys Val Leu Cys Leu
10 380 385 390

TGAGGCACCC CCAGGACAGC ACACGGTGAG GGTGCGGGGC CTGCAGGCCA GTCCCACGGC
1264

15 TCTGTGCCCG GTGCCATCTT CCATATCCGG GTGCTCAATA AACTTGTGCC TCCAATGTGG
1324

AAAAAAAAAAA AAAAAAAAAC TCGAG
1349

20 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35 (A) NAME/KEY: CDS
 (B) LOCATION: 29..265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40 GAATTCTGGCA CGAGTGCAGG CGCGCGTC ATG GCT GCT TTG AGA CAG CCC CAG
40 52

 Met Ala Ala Leu Arg Gln Pro Gln
 1 5

5 GTC GCG GAG CTG CTG GCC GAG GCC CGG CGA GCC TTC CGG GAG GAG TTC
100
Val Ala Glu Leu Leu Ala Glu Ala Arg Arg Ala Phe Arg Glu Glu Phe
10 10 15 20

10 GGG GCC GAG CCC GAG CTG GCC GTG TCA GCG CCG GGC CGC GTC AAC CTC
148
Gly Ala Glu Pro Glu Leu Ala Val Ser Ala Pro Gly Arg Val Asn Leu
25 30 35 40

15 ATC GGG GAA CAC ACG GAC TAC AAC CAG GGC CTG GTG CTG CCT ATG GCT
196
Ile Gly Glu His Thr Asp Tyr Asn Gln Gly Leu Val Leu Pro Met Ala
45 50 55

20 CTG GAG CTC ATG ACG GTG CTG GTG GGC AGC CCC CGC AAG GAT GGG CTG
244
Leu Glu Leu Met Thr Val Leu Val Gly Ser Pro Arg Lys Asp Gly Leu
60 65 70

25 GTG TCT CTC CTC ACC ACC TCT TAGGGTGCCG ATGAGCCCCA GCGGCTGCAG
295
Val Ser Leu Leu Thr Thr Ser
75

30 TTTCCACTGC CCACAGCCCCA GCGCTCGCTG GAGCCTGGGA CTCCTCGGTG GGCCAATAT
355
GTCAAGGGAG TGATTCAAGTA CTACCCAGCT GCCCCCCCTCC CTGGCTTCAG TGCAGTGGTG
415

35 GTCAGCTCAG TGCCCCCTGGG GGGTGGCCTG TCCAGCTCAG CATCCTTGGGA AGTGGCCACG
475

40 TACACCTTCC TCCAGCAGCT CTGTCCAGAC TCGGGCACAA TAGCTGCCCG CGCCCAGGTG
535
TGTCAGCAGG CCGAGCACAG CTTCGCAGGG ATGCCCTGTG GCATCATGGGA CCAGTTCATC
595

5 TCACTTATGG GACAGAAAGG CCACCGCCTG CTCATTGACT GCAGGTCCCTT GGAGACCAGC
655

CTGGTGCCAC TCTCGGACCC CAAGCTGGCC GTGCTCATCA CCAACTCTAA TGTCCGCCAC
715

10 TCCCTGGCCT CCAGCGAGTA CCCTGTGCGG CGGCGCCAAT GTGAAGAAGT GGCCCGGGCG
775

15 CTGGGCAAGG AAAGCCTCCG GGAGGTACAA CTGGAAGAGC TAGAGGCTGC CAGGGACCTG
835

GTGAGCAAAG AGGGCTTCCG GCGGGCCCGG CACGTGGTGG GGGAGATTG GCGCACGGCC
895

20 CAGGCAGCGG CCGCCCTGAG ACGTGGCGAC TACAGAGCCT TTGGCCGCCT CATGGTGGAG
955

AGCCACCGCT CACTCAGAGA CGACTATGAG GTGAGCTGCC CAGAGCTGGA CCAGCTGGTG
1015

25 GAGGCTGCGC TTGCTGTGCC TGGGGTTAT GGCAGCCGCA TGACGGGCGG TGGCTTCGGT
1075

30 GGCTGCACGG TGACACTGCT GGAGGCCTCC GCTGCTCCCC ACGCCATGCG GCACATCCAG
1135

GAGCACTACG GCGGGACTGC CACCTTCTAC CTCTCTCAAG CAGCCGATGG AGCCAAGGTG
1195

35 CTGTGCTTGT GAGGCACCCC CAGGACAGCA CACGGTGAGG GTGCGGGGCC TGCAGGCCAG
1255

TCCCACGGCT CTGTGCCCGG TGCCATCTTC CATATCCGGG TGCTCAATAA ACTTGTGCCT
1315

40 CCAATGTGGA AAAAAAAA AAAAAAAACT CGAG
1349

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7676 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 CCGAGCATCC CGCGCCGACG GGTCTGTGCC GGAGCAGCTG TGCAGAGCTG CAGGCGCGCG
60TCATGGCTGC TTTGAGACAG CCCCAGGTAG CGGAGCTGCT GGCGGAGGCC CGGCGAGCCT
12025 TCCGGGAGGA GTTCGGGGCC GAGCCCGAGC TGGCCGTGTC AGCGCCGGGC CGCGTCAACC
180TCATCGGGGA ACACACGGAC TACAACCAGG GCCTGGTGCT GCCTATGGTG AGGGGCTGCA
30 240CGGGGAGCCC CTAGCCCCGCC GCCGCCTGTC CCGGTGGCCG AGGAGGGCGG GCCTCGGGGA
30035 CGCTGGGGC GAGTTCTTCC CGCGGGAGAT GTGGGGCGGG CAGCTGCGCC TGGAGCACCG
360GTGCACGGAA GAGTCCCCGG GACAGGCTGT TCCCCACGTT GGAAGGGAGG AAGCGAAGAA
42040 GTGGTCCCCA GAGGGTGCAG GGCGCGCTCT TGGCTCAAGC CCGCCCTCTG GGGGCTGGGG
480

5 CTCCTCGCCT TCAACCTGGG AGCATGTTCC CCTTAAACTG TGAGGCCCTG TGTGCCACGC
540

AGAAGGGGAC ACTCCGCGCC TCCGGCCACC GTGGGGCCCC AACCGCAGAC CTGGGCGAAC
600
10 GTAGCCTTCT GGCCCAGCCC GTTCAATTAA CAGAGGAGGA AACTGAGGCC TAGAGAGGCC
660

CAGTGAACCTG CTGGAGGTCA CACAGCAGGT TCTTGGCGGG GCTGCGACTT GGGAGTGAGG
15 720

ACTCCCAGCT TTCAGCGGGG GGCGCTTTCC GCCCCATCTG CAGCTTGGGG AGTGCACAGG
780

20 TACAGGATGT CCAGAGCCAC CCAAAATGTA AAGGCTTTGG AGCTCCAGTG ATCTGTTTC
840

CCTTTGGGCT AAGCTCTCCC CCCTTGGCCC ACAGCTCAGG GCAGAGTCCA GGTCTGTGCT
900
25 CCAGCTGCAG CCGCCCCGCC CCTGAAGACC TAAGGGGGCA GGGCTCAAGC CCCCAAGGTC
960

AGCTGGCCCT CAGGATCTTC CCTGCGACGC TGAACCTGGA GGTCAGAAC CTGATGACTG
30 1020

TGGAGGCATC AGAACCTCGG CTGGAGGCAG TGTCAATTGGA GAGGCTTACT CCAGCTGGCG
1080

35 GAAGCCTCAC GTACTGCTTG TCTCTCCTGC CAGGCTCTGG AGCTCATGAC GGTGCTGGTG
1140

GGCAGCCCCC GCAAGGATGG GCTGGTGTCT CTCCTCACCA CCTCTGAGGG TGCCGATGAG
1200
40 CCCCCAGCGGC TGCAGTTCC ACTGCCACCA GCCCAGCGCT CGCTGGAGGCC TGGGACTCCT
1260

5 CCGTGGGCCA ACTATGTCAA GGGAGTGATT CAGTACTACC CAGGTATGGG GCCCAGGCCT
1320

GAGCCAAGTC CTCACTGATA CTAGGAGTGC CACCTCACAG CCACAGAGCC CATTCAATTG
1380

10 TCTGATACAC TGTGGGAAAG GCTTGTAGAG TGGAGCATCC CATTGTACAG ATGAGGAAAC
1440

TGATGCCCCC AGAAGGTCGG GAACTGCCCT TGGGTTCCCG GTGACCTGAT TGGAGGAGCC
15 1500

AGGATTGAA CCCCAGCCTT TTTCCCTCC AGAGCCCTAA ACCAGGAGGA CAATTAGAAG
1560

20 TGTCCCAGCA ACCTCAGAGG GTGGGAAAAT GGAGGGAGT GGGTCCCTTG GGCCAGCAGG
1620

TTGGTGGGTT TCTTGACAAT TGAGACACAC ACCTAGAAAC AGTTGCTAGG CCGTTGCTGC
1680

25 CCTTCCCGCC AGGACACCTG CCCTTCCTGT CCAATCCTCC CAGGCAGCCT CTCTTACCAT
1740

CACCTGTTCT TTCCCCCTGC AGCTGCCCCC CTCCCTGGCT TCAGTGCAGT GGTGGTCAGC
30 1800

TCAGTGCCCCC TGGGGGGTGG CCTGTCCAGC TCAGCATCCT TGGAAAGTGGC CACGTACACC
1860

35 TTCCTCCAGC AGCTCTGTCC AGGTACCAGC TAGGCCAG CCCTGACCCA GCCCTCCTTC
1920

CCTGAGGTCT CCAGGTGGTC CCAGCTTCTA CTATGCCTTA TGGAGGGGGT GGCAGGGAAT
1980

40 CTCCCTGGAG TGTCATTGAA GCCACTGCTG CTTCCACCAG CCCTAGCCTC CCCACCTCAC
2040

5 CCTGTACTGC AGACTCGGGC ACAATAGCTG CCCGCGCCCA GGTGTGTCAG CAGGCCGAGC
2100

ACAGCTTCGC AGGGATGCCA TGTGGCATCA TGGACCAGTT CATCTCACTT ATGGGACAGA
2160

10 AAGGCCACGC GCTGCTCATT GACTGCAGGT TGGGCTCGCT CCCCTCGTCC CCTCCCCGCC
2220

TGCACTCAGC AGCTCCTGGG TGGAGTGTGC CCACTGCCTG GCGCAGCAAG CACACGCTTG
15 2280

GCCTCGTCAT CTCCCCCATT GTAATCCAC CCCAGGTCTT TGGAGACCAAG CCTGGTGCCA
2340

20 CTCTCGGACC CCAAGCTGGC CGTGCTCATC ACCAACTCTA ATGTCCGCCA CTCCCTGGCC
2400

TCCAGCGAGT ACCCTGTGCG GCGGCCAA TGTGAAGAAG TGGCCGGGC GCTGGGCAAG
2460

25 GAAAGCCTCC GGGAGGTACA ACTGGAAGAG CTAGAGGGTG AGAACTGCCA GGGTGCTCTA
2520

TCCTGGAGGC GGCTGTGCTC CCTGCTGGCG CCTCAGTGTG GCCTTGACCC TGCCTGGGAC
30 2580

CCCGATCTCC AGGGGCTTCT GCCATGCTCT CCCCAGTCCC TTCAAACACT GCGCACCCAG
2640

35 GGTTCCAATC TCAGCAGGGG TGCTTGAAAT CCTAAAATGG TCTTATCTAA TCAGAAAAAT
2700

CATGTTCCA TTGTGGAAAA TGTAGAAAAG TACAAAGTAG AAAATAATAA GCTATAAGGG
2760

40 CACTACCCAG AGATAGGCAC TGCTGACATT TTCACGTTTC CTTTCAGTAT TTTCCACAT
2820

5 CTGTCTCAA AGCTGAGTAT ATGTAATATA TCATCACTTT CCCCCCCCAC CCCCTTTTT
2880

TTAAGAGGCA GGGTCTCATT CTGTTGCCA AGCTGGAGTG TAGTGGTGTG ATCATAGCTT
2940

10 ACTGCAAAC TGAACCTTTG AGCTCAAGGG ATCCTCCAG CTCAGCCTTC CAAGTAGCTG
3000

AGATTACAGG TGTGCCACCA TGCCCGGCTA ATTTTATCT TCGTAAAGAC GGCTTGTAG
15 3060

TGTTGCCAG GATGATCCTG AACTCTGCC TCAAGAGGTC CTCCGCCTT GGGCTCCAA
3120

20 AGTGTGGGA TTATAGGCAT GAGCCACTGC GGCCAGCCA TTTGCCGTGT TTTTTTTTG
3180

GACACAGAGT TTCGGTCTTG TCACCCATGC TGGAGTGCCTA TGGTGCATC TCAGCTCACT
3240

25 GTAACCTCTG CCTCCCGGGT TCAAGTGATT CTCCGCCTC AGCCTCCGA GTAGCTGGGA
3300

CTACAGGCGC CCGCCACTAC GCCTGGCACA TTTTTATAG TTCTAGTAGA GACTGGGTT
30 3360

TCACCATGTT GCCCAGGCTG GTCTCAAACG CCTGACCTCA GGTGATCCTC CCGCCTCAGC
3420

35 CTTCCAAAGT GCTGGGATTA CAGGCAGTGAG CCATAGTGCC GGTCTCTTT TTTTTTTT
3480

TTAAACTAAA CATAATCTCA GAACCCAGAA CCCTATCTTA TCTTATGCCA TGAAAGGCAT
3540

40 ATCTCGGCCTG GGCTCTTTT TTTTTTTT CTTTTTTT GGGCGAGGTG GAGGCTTGCC
3600

5 CTGTTGCCCA GGCTGGAGTG CAGCGCGCA ATCTCGGTTC ACTGCATCCT CCACCTCCTG
3660

GGTCCAAATG ATCCTCCTGC CTTAGCTTCC TGAGTAGGTG GGATTACTGG AACCCACCAC
3720

10 CACGCCAGC CAATTTTAT ATTTTAGTA GAGACGGGGT TTCATGTTGG CCAGGCTGGC
3780

15 CTCGAACCTCC TGACCTCGTG ATCTGCCCGC CTCAGCCTCC CAATGTGCTA GGATTACATG
3840

TGTGAGCCAC TGCACCTGGC CTCCGTGTGG CTCTTAAAG CTCCACAATA TTTTAGCATT
3900

20 CAGGTGCTCT GTCATTTACT TAACTATTT CTGATACACC TCACACTGCG ATTAACTTTC
3960

CTTATTTATC TTTTTATTA TTTATTTATT TATTTATTTG AGACAGAGTC TTGCTCTGTC
4020

25 ACCCAGGCTG GAGTGCAGTG GCACGATCTC GGCTCACTGC AACCTCTGCC TCCCAGGTTTC
4080

AAGTGATTCT CCTGCCTCAG CCTCCTGAGT AGCTAGGATT AGAGGCATGT GCCACCACAC
30 4140

CTGGCTAACATC TTCGTATTT TAGCAGAGAT GAGGTTTAC CATGTTGGTC GGGCTGGTC
4200

35 TGAACTCCTG ACCTGGTGAT CTGCCACCT CAGCCTCCCA AAGTACTGGG ATGACAGGCA
4260

TGAACCACTG TGCCTGGCCA TCTTTTTAT TTTTAAAGA GATGGGTTCT GCTAAGTTGC
4320

40 CCAGGCTGGA CCTGAACTCT TGGGCTCAAG TAATCTTCTC ACCTAGTCTC CTGGGTAGCT
4380

5 GCAACCAAAG GCACCCGGTT TATCTGCATT CTCTTTTTT TCTTTGAGAC TGAGTCCTGC
4440

TCTGTAGCCC AGGCTGGAGC GCAGTGGCGT GATCTCGGCT CACTGCAACC TCCGTCTTCA
4500

10 GGGTTCAAGC AATTCTCCTG CCTCAGCCTC TGGAGTGGCT GGGACTACAG GCGTGTGCCA
4560

CCAGAGCGAG TTAATTTTTT TTTTTTTTG TATTTTTAGT GGACACTGGG TTTCACTATA
15 4620

TTGCCAGGC TGGTCTTGA CTCCTGACCT CAAGTGATCC GCCTGCCTTG GCCTCCAAA
4680

20 GTGCTGGGAT TACAGGCACA GGCGTGAGCC ACTACACCTG GCCTATCTGC ATTCTCTTAA
4740

TAGTTCTTA GAAATGGATT CTTAGGAGTA GGATTACAGA GTCAAGAGAC ACAAGTTTG
4800

25 TAGGCTGGGT GCGGTGGCTC ACGTCTGTGC CTGTAATCCC AGTACTTTAG GAGGCCAAGG
4860

TGGGCAGATT CATTGAGCTC AGGAATTCGA GACCAGCCTG GGCAACATGG CAAAACCCCA
30 4920

TCTCTAAAGA AATACAAAAAA TTAGCCAGGT GTGGTGGTGT GTGCCTGTAG TCCTAGCTAC
4980

35 TTAGGAGGCT GGGGTGGGAG GATCAATTGA GCCCAGGAGG TTGAGACTGC AGTGAGCTGT
5040

GATTGCACCA TGGCACTCCA GCCTGGGCCT CAAAGTGAGA TCCTGTCTCC AAAACAAAAAA
5100

40 AGATACAAGT ATCCTTAAGG CTCCTGCTAC ACATGGCCAG GAAGGTAGTC TATTGGACAG
5160

5 TTTTAAGGTC ATTATCAATA TTAGCTCATT TAATTCCCTC CAAAACCTTG TAAAGCACAT
5220

10 TCTGCTACCA TAGTTGTCAT ATTTTGATG GGGGAATCTA CAGTGAGAGG CAGTGCTGGG
5280

15 ATCTGAACCC CATCTGGACA GATTAGCTCC AGGGCCCATG CTCTTGACTG GCTGGCCGCG
5340

20 CTGCCACAC TGAGTTGTTG CTTCCTGGCA GGGTAGGTGT GCCTATCTCA GGGACACTAG
5400

25 ACAGCTCCGA GGGACCTCCC TGTCCTTTTC CTTTGTGAAC TGTGTCACGT TCTCCAGAGC
5460

30 AGGGCTCAGA CCTGCCCTGC CTGCTCTGTG CAGATGCCCT TGGCCAAGGT TTTCACACTG
5520

35 GAACAAAGTTG GTCCCTCCTC CCCACCCCCAG CCTGTCCCTTG GCCCTCCTCC AGGTCTCCTT
5580

40 CTGCATAGGA GCAGCTCACC CTGCCTCCTC CAGAGTCCTG CCCTAGAAC GCAATCCCTC
5640

45 TCCTTCCATC CCCTGCCTGG CTGCCTGGCT CCTTCCCTCA GCCTCCAAGA CATGCTCAGT
5700

50 TTTCTTCCCT CCTAAAACAC CACCCACTGT CTCATTTCCA TTCATTTCTT TCTTTCTTTC
5760

55 TTTCTTTTTT TTTTTGAGA GGGAGCCTCA CTCTGTCACC CAGGCTGAAG TGCAGTGGCA
5820

60 TGATCTCCAC TCACTGCAAC CTCCGCCTCC CAGGTTCAAG CAATTCTCCT GCCTCAGCCT
5880

65 CCTGAGTAGC TGGGATTACA GGCGCCTGCC ACGATGCCCG GCTAACCTTT GTATTTTAG
5940

5 TAGAGACGGG GTTTCGCCAT GTTGGCCAGG CTGGTCTCGA GCTCCTGACC TCAGGCAATC
6000

TGCCTGCCTC AGCTTCCCAA AGTGTGGGA TTACAGGTGT GAGCCACCGC GCCCACCCAT
6060

10 TCATTTCTCA GTCCCTTGAA TCTACTTGCC CCTCCATCCC GCCATGCCAC CTACCCCTAAC
6120

AACCTCCCCC CTTAAACCTG CGGGTTGGC CGGGCGCAGT AACTGAGTC AGTACTGGTA
15 6180

CTGACCCAGG TACCCCTCCA GCCTCAGCTC CAGTCAGATG GGACAGCCTG CTGGTCCCTG
6240

20 GCTGCTTCTG CCCCTCTTC TGGAGCCCCA GCCCTGGAGG CTCCATGTGG CTCAGCAGAA
6300

CTTCTCTCC TCCTGCTCTG TGGTGGCCTC TTGAGGGCAG CACTCACCTT GGAAAGCATG
6360

25 GAGTGTTCACCA ACCCTCACTG CTCCCTGAAG GACCAAGGTG TCCCATTAA CAGTCGGGG
6420

AGGAGGCAGT GTGATAAAGG GGCTCTTCAG ACCCACGTCT GAGAGAGCCA GGCTGCGCCG
30 6480

CCCCCGCGGC CTTCCACCCCT TCACCGTCCA GCCAGGGCCA CTGCCATCAC CGCCTGCTGG
6540

35 TCCTCACAGG CGTCGGGGCC CCAGGCAGTG AGAAGGCAGC TGCTGACTCC TCTTCCTCC
6600

CCAGCTGCCA GGGACCTGGT GAGCAAAGAG GGCTTCCGGC GGGCCCGGCA CGTGGTGGGG
6660

40 GAGATTCGGC GCACGGCCCA GGCAGCGGCC GCCCTGAGAC GTGGCGACTA CAGAGCCTT
6720

5 GGCCGCCTCA TGGTGGAGAG CCACCGCTCA CTCAGGTGAG GCCCTCTGGG CGCCCCGCTC
6780

10 CTGCCGGGCA CAGGCCGGCC CAGGCCACC CCTTCAATAT CCTCTCTGCA GAGACGACTA
6840

15 TTATGGCAGC CGCATGACGG GCGGTGGCTT CGGTGGCTGC ACGGTGACAC TGCTGGAGGC
6960

20 CTCCGCTGCT CCCCACGCCA TGCGGCACAT CCAGGTGGGC GGGCACCAGG GCCTGGCGG
7020

25 GCAGGAGCGG CAGCTTCCCG GGGCCCTGCC ACTCACCCCC AGCCCGCTC TTACAGGAGC
7080

30 ACTACGGCGG GACTGCCACC TTCTACCTCT CTCAAGCAGC CGATGGAGCC AAGGTGCTGT
7140

35 GCTTGTGAGG CACCCCCAGG ACAGCACACG GTGAGGGTGC GGGCCTGCA GGCCAGTCCC
7200

40 ACGGCTCTGT GCCCGGTGCC ATCTTCCATA TCCGGGTGCT CAATAAACTT GTGCCTCCAA
7260

45 TGTGGTACCT GCCTCCTCTA GAGGTGGGTG TATGCTTGGG TGTCAGAGAA TGGGGGATGT
7320

50 CAGAACCGCT CCCCTACCCCT AGGGGAGCAC CTCTCAGGCC CCAGAAGAAT GGGCAAGGCA
7380

55 GGGCCTAGCA GTAGCAAAAC CATTATTAAC GTGCAGAACAA AAGGCTGGGT CCTTGTGCTG
7440

60 CTCCCAGCTC TTTGGTTACA AATAGGTTTG GGCCCACAGA GGACGGACCT TGCCCCCTTC
7500

5 ATGCCTCCC GGAGACACCT AGCCCCCTGCT CTGTGCATGC GGGTGGGCTG GGCCCCCAGG
7560

GGTGCAAGGA TGGAGTAGCT GAGGGAGGCTC CGGGAGAGGA GTCGGGAGGA CGCCTAGTGG
7620

10 GACATTGCGG GGGTGGCGCA GGGTGGGTC AAGTTGGAA GAAACTGTTG GGTCCA
7676

(2) INFORMATION FOR SEQ ID NO:8:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTTCCGG GAGGAGTTCG G
30 21

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTTGTAG TCCGTGTGTT C

21

10 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 GCCAGCAGCT CCGCGACCTG G

21

(2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTTCCTCCC TTCCAAACGTG G

21

5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

20

CCCAGGGCTCC AGCGAGCGCT G

21

(2) INFORMATION FOR SEQ ID NO:13:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

40 21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCACAGCTC AGGGCAGAGT C
21

20 (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35 GGACACTTCT AATTGTCCTC C
21

(2) INFORMATION FOR SEQ ID NO:16:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATGAACTGG TCCATGATGC C

21

15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

30

AGGGGGCACTG AGCTGACCAC C

21

(2) INFORMATION FOR SEQ ID NO:18:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACTTCTACA CATTGGCGCC G
10 21

(2) INFORMATION FOR SEQ ID NO:19:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTCGCAGGG ATGCCCTGTG G
21

30 (2) INFORMATION FOR SEQ ID NO:20:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 TCATCACCAA CTCTAATGTC C
21

(2) INFORMATION FOR SEQ ID NO:21:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTCAGCAGT GCCTATCTCT G

21

25 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

40 AGCAGCGGAG GCCTCCAGCA G
21

(2) INFORMATION FOR SEQ ID NO:23:

5

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

20 CCTCACCGTG TGCTGTCCTG G
21

(2) INFORMATION FOR SEQ ID NO:24:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTGCGCTT GCTGTGCCTG G
21

40 (2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid

- 5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

15 CCTCACCGTG TGCTGTCCTG G
21

(2) INFORMATION FOR SEQ ID NO:26:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCACCGTG TGCTGTCCTG G

21

35 (2) INFORMATION FOR SEQ ID NO:27:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGGACTGC CACCTTCTAC C
21

15 (2) INFORMATION FOR SEQ ID NO:28:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30 CTCAATAAAC TTGTGCCTCC A
21

(2) INFORMATION FOR SEQ ID NO:29:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGGATATGGA AGATGGCACC GGG

23

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGAGCTGCAG GCGCGCGTCA TG

22

(2) INFORMATION FOR SEQ ID NO:31:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGAGCATCC CGCGCCGAC

19

5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTGCCCG CCCCCACATCT

20

5

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule encoding human genomic galactokinase, said nucleic acid molecule selected from the group consisting of:
 - 10 (a) a nucleic acid molecule comprising the sequence as set forth in SEQ ID NO:7; and
(b) a nucleic acid molecule differing from the nucleic acid molecule of (a) in codon sequence due to the degeneracy of the genetic code.
 - 15 2. A vector comprising the nucleic acid molecule of claim 1.
 3. A recombinant host cell comprising the vector of claim 2.
 4. An isolated nucleic acid molecule comprising a DNA sequence that encodes 20 nucleotides 29 to 1204 of SEQ ID NO:5 or nucleotides 29 to 265 of SEQ ID NO:6.
 5. A vector comprising the nucleic acid molecule of claim 4.
 6. The vector according to claim 5 which is a plasmid.
 - 25 7. A recombinant host cell comprising the vector of claim 5.
 8. A process for preparing a human galactokinase protein comprising culturing the recombinant host cell of claim 7 under conditions promoting expression 30 of said protein and recovery thereof.
 9. An isolated protein encoded by the DNA sequence of claim 4.
 10. A monoclonal antibody that is specifically reactive with the protein of 35 claim 9.
 11. A method for diagnosing conditions associated with human galactokinase deficiency which comprises isolating a serum or tissue sample from an individual; allowing such sample to come in contact with an antibody or antibody fragment

5 which specifically binds to the human galactokinase protein of claim 9 under conditions such that an antigen-antibody complex is formed between said antibody or antibody fragment and said galactokinase protein; and detecting the presence or absence of said complex.

10 12. A method for diagnosing conditions associated with human galactokinase deficiency which comprises isolating a nucleic acid sample from an individual; assaying said sample and the DNA sequence, or corresponding RNA sequence, that encodes a human galactokinase gene; and comparing differences between said sample and said DNA (or RNA) that encodes nucleotides 29 to 1204 of SEQ ID NO:4, wherein said
15 differences indicate mutations in the human galactokinase gene.

13. The method of claim 12 wherein said sample is RNA which is subsequently amplified by PCR-RT.

20 14. The method of claim 13 wherein assaying said sample comprises a restriction endonuclease digestion.

15. The method of claim 14 wherein said restriction endonuclease is Msc I.

25 16. The method of claim 12 wherein assaying said sample comprises a hybridization assay.

30 17. The method of claim 16 wherein the hybridization assay is heteroduplex electrophoresis which comprises determining differential mobility of heteroduplex products in polyacrylamide gels, said heteroduplex products are the result of hybridization between the nucleic acid sample and the DNA sequence, or corresponding RNA sequence, that encodes nucleotides 29 to 1204 of SEQ ID NO:4.

35 18. The method of claim 12 wherein assaying said sample comprises gel electrophoresis of restriction fragment length polymorphisms of said nucleic acid sample and the DNA sequence, or corresponding RNA sequence, that encodes nucleotides 29 to 1204 of SEQ ID NO:4.

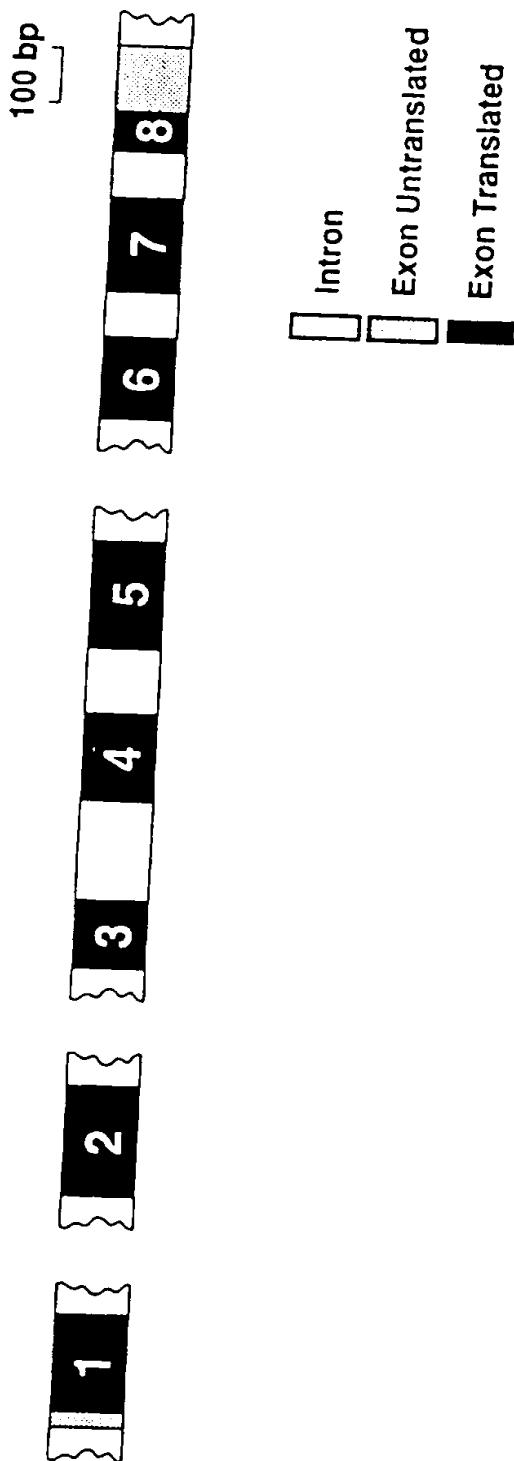
5 19. The method of claim 12 wherein assaying said sample comprises DNA sequencing.

10 20. A method for diagnosing conditions associated with human galactokinase deficiency which comprises isolating cells from an individual containing genomic DNA and assaying said sample by *in situ* hybridization using the DNA sequence that encodes nucleotides 29 to 1204 of SEQ ID NO:4, nucleotides 29 to 1204 of SEQ ID NO:5, or nucleotides 29 to 265 of SEQ ID NO:6; or a fragment that encodes at least one exon of said sequence; or a fragment containing at least 15 contiguous base pairs of said sequence as a probe.

15

21. A transgenic non-human mammal capable of expressing in any cell thereof the DNA of claim 4.

Figure 1



SUBSTITUTE SHEET (RULE 26)

FIGURE 2(a)

S
 CCGAGCATCCCGCGCCCACGGGTCTGTGCCGGAGCACCTGTGCAGAGCTGCAGGGCGCG
 TCATGCGCTGCTTGTAGACACCCCCAGGTGCCGGAGCTGCTGGCCAGGGCCCGGGAGCCT 1
 M A A L R Q P Q V A E L L A E A R R A 58
 TCCGGGAGGAGTTCCGGGGCCGACCCCCAGCTGGCGTGTCAAGGCCGGGGCGTCACC 118
 F R E E F G A E P E L A V S A P G R V N
 TCATCGGGGAACACACGGACTACAACCAGGGCTGGTGTGCCATGGTACGGGCTGCA 178
 L I G E H T D Y N Q G L V L P M
 CGGGGAGCCCTAGCCGUCCGCCCTGTCCCGTCGCCAGGAGUCGGGGCTCGGGGA 238
 CGCTGGGGCGAGTTCTTCCCAGGGAGATGTGGGCGGGCAGCTCCGCTUGAGCACCG 298
 GTGCACGGAAAGACTCCCCGGGACAGGCTGTTCCCACGTTGGAAAGGGAGGAAGCGAAGAA 358
 GTGGTCCCAGGGTGCGCGGGCCTCTGGCTCAAGGCCGCCCTCTGGGGCTGGGG 418
 CTCTCGCCCTCAACCTGGGAGCATGTTCCCCCTTAAACTGTGAGGCCCTGTGTGCCACGC 478
 AGAAGGGGACACTCCGCGCTCCGGCACCGTGGGGCCCAACCGCACGACCTGGCGAAC 538
 CTAGCCTCTGGCCCAGCCGTTCAATTACAGAGGAGAAACTGAGGCCCTAGAGAGGCC 598
 CAGTGAACCTGCTGGAGGTACACAGCAGGTTCTGGCGGGCTGCACCTGGAGTGAGG 658
 ACTCCCAGCTTCAAGGGGGGGCGTTCCGCCCATCTGAGCTGGGAGTGCACAGG 718
 TACAGGATGTCCAGAGCCACCCAAATGTAAGGCTTGTGAGCTCCAGTGTATCTGTTTC 778
 CCTTTGGGCTAAGCTCTCCCCCTTGGCCCACAGCTCAGGGCAGACTCCAGGTCTGTCT 838
 CCAGCTGCAGCCGCCCGGGCTGAAGACCTAAGGGGGCAGGCTCAAGCCCCAAGGTC 898
 AGCTGGCCCTCAGGATCTTCCCTGGCACGCTGAACCTGGAGGTTCAAGAACCTGATGACTG 958
 TGAGGCATAGAACCTGGCTGGAGGAGTGTCAATTGGAGAGGCTTACTCCAGCTGGCG 1018
 GAAGCCTCACGTACTGCTTGTCTCTGCCAGGCTCTGGAGCTCATGACGGTGTGGTG 1078
 A L E L M T V L V
 GGCAGCCCCCGCAAGGATGGGCTGGTGTCTCTCTCACCAACCTCTGAGGGTCCCCATGAG 1138
 G S P R K D G L V S L L T T S E G A D E
 CCCCAGGGCTGCAGTTCCACTGCCACAGCCAGCGCTCGCTGGACCCCTGGACTCCT 1198
 P Q R L Q F P L P T A Q R S L E P G T P
 CGGTGGGCCAACTATGTCAGGGAGTGATTCACTACCCAGGTATGGGGCCAGGCCT 1258
 R W A N Y V K G V I Q Y Y P
 GAGCCAAGTCTCACTGATACTAGGAGTGCCACCTCACAGCCACAGAGCCATTGATTG 1318
 TCTGATAACACTGTGGGAAGGCTTGTAGAGTGAGCATCCATTGTACAGATGAGGAAC 1378
 TGATCCCCCAGAAGGTGGAACTTGCCCTGGGTTCCCGTACCTGATTGGAGGAGCC 1438
 AGGATTTGAACCCCAGCTTTTCTCCCTCCAGAGCCCTAAACCAGGAGGACAATTAGAAG 1489
 TCTCCAGCAACCTCAGAGGGTGGAAAATGGAGGGAGTGGTCCCTGGCCACSCAGG 1558
 TTGGTGGGGTCTTGACAATTGAGACACACACCTAGAAACAGTTGCTAGGCCCTTGTSC 1618
 CCTTCCGCCAGGACACCTGCCCTCTGTCCAATCTCCAGGCACTCTTACCAT 1678
 CACCTGTTCTTCCCCCTGCAGCTGCCCTGGCTTCAGTGCAGTGGTGGTCAGC 1738
 A A P L P G F S A V V V S
 TCAGTCCCCCTGGGGGTGCCCTGTCCAGCTAGCATCTTGGAAAGTGGCCACGTACACC 1798
 S V P L G G G L S S S A S L E V A T Y T
 TTCTCCAGCAGCTCTGTCCAGGTACCACTAGGCCCCAGCCCTGACCCAGCCCTCTTC 1858
 F L Q Q L C P
 CCTGAGGTCTCAGGTGGTCCAGCTTACTATGCTTATGGAGGGGGTGGCAGGAAAT 1918
 CTCCCTGGAGTGTCAATTGAAGCCACTGCTGCTTCCACCAGCCCTACCCCTCCCCACCTCAC 1978
 CCTGTACTGCAGACTCGGGCACAACTAGCTGCCGGGGCAGGTGTGTCAGCAGGGCGAGC 2038
 D S G T I A A R A Q V C Q Q A E
 ACAGCTTCCAGGGATGCCCTGTGGCATCATGGACCAAGTTCACTCACTTATGGGACAGA 2098
 H S F A G M P C G I M D Q F I S L M G Q
 AAGGCCACGGCTGCTCATTGACTGCAGGTTGGCTCGCTCCCTGTCCTCTCCGCC 2158
 K G H A L L I D C R

FIGURE 2 (b)

TGCCACTCAGCAGCTCUTTWWGGACTGTGCCCACGTGCTGGCGAGCAAGCACACGCTTG 2218
 GCGTCGTATCTCCCCATTTAACTCACCCAGGTCTTGGAGACCAGCCTGGTGC~~A~~ 2278
 S L E T S L V P

CTCTCGGACCCAAAGCTGGCGTGCTCATCACCAACTCTAATGTCCGCCACTCCCTGGCC 2338
 L S D P R L A V L I T N S N V R H S L A

TCCAGCGAGTACCCGTGCGGGCGGCCAATGTGAAGAAGTGGCCGGCGCTGGCAAG 2398
 S S E Y P V R R R Q C E E V A R A L G K

AAAAAGCCTCCGGAGGTACAACCTGGAAAGAGCTAGAGGGTAGAGAACTGCCAGGGTCTA 2458
 E S L R E V Q L E E L E

TCTGGAGCCGGCTGTGCTTCTCTGCCTAGTGTCGGCTTGACCTGCCTGGGAC 2518
 CCCGATCTCCAGGGCTTCTGCCATGCTCTCCCAAGTCCCTAACACTGGCACCCAG 2578
 GTTCCAATCTCAGCAGGGCTGCTGAATCCTAAATGTCCTTATCTAACTAGAAAAAT 2638
 CATGTTTCAATTGCAAATGTAAGAAAATACAAAGTAGAAAATAAAGCTATAAGGG 2698
 CACTACCCAGAGATAGGCACTGCTGACATTTCACGTTCTTCAGTATTTCACAT 2758
 CTGTCCTCAAAGCTGACTATATGTAATATATCATCACTTTCCCCCCCCACCCCCCTTTT 2818
 TTAAGAGGCAGGGCTCATTCGTTGCCAAGCTGGAGTGAGTGGTGTGATCATAGCTT 2878
 ACTGCAACTTGAACCTTGAAGCTCAAGGGATCCTCCAGCTCAGCCTTCAAGTAGCTG 2938
 AGATTACAGGTGTGCCACATGCCCGCTAATTTCATCTCGTAAAGACGGCTTGTAG 2998
 TCTGCCCAGGATGATCCGAACCTCTGGCTCAAGAGGTCTCTGCCCTGGCTCCAA 3058
 AGTGTGGGATTATAAGGCATAGGCCACTCGGGCCAGGCCATTGCGTGTTTTTTTTG 3118
 GACACAGGTTTGGCTCTTCACCCATGCTGGAGTCCAAGTGGTGCATCTCAGCTCACT 3178
 GTAACCTCTGCCCTCCGGGTTCAAGTGATTCTCGGCTCAGCCTCCAGTACGCTGGG 3238
 CTACAGGCCCGGCAACTAACGCTGGCACATTTCATAGTCTAGTAGAGACTGGGTT 3298
 TCACCATGTTGGCCAGGGCTGGCTCAAAACGCTGACCTCAGGTGATCCTCCCCCTCAGC 3358
 CTTCCAAAGTGTGGGATTACAGCGTGAAGCCATAGTCCGGTCTCTTTTTTTTTTG 3418
 TTAAACTAAACATAATCTCAGAACCCAGAACCCCTATCTTATCTTATGCCATGAAAGGCAT 3478
 ATCTGGCTGGCTCTTTTTTTTTCTTTTTGGGAGGGCTTGTGGGAGGTGGAGGCTTGCC 3538
 CTGTTGCCAGGTGGAGTGCAGCGGCGCAATCTCGGTTACTGCATCCTCACCTCCTG 3598
 GCTCCAATGATCTCTGCCCTAGCTTCTGAGTAGCTGGGATTACTGGAACCCACAC 3658
 CACGCCAGCCAATTTCATTTAGTGGAGACGGGTTCTAGTGGCCAGGCTGGC 3718
 CTCGAACCTCTGACCTCTGACTCTGCCCTCAGCTCCCTGAGTAGCTAGGATTACATG 3778
 TGTGAGCCACTGCACCTGCCCTCGTGTGGCTCTTAAAGCTCCACAATTTCAGCATT 3838
 CAGGTGCTGTCAATTAACTATTCTGATAACCTCACACTGCAGTAACTTTC 3898
 CTTATTATCTTTTTATTATTATTTATTATTTATTGAGACAGAGTCTGCTCTGTC 3958
 ACCCAGGCTGGAGTGCAGTGGCACGATCTGGCTCACTGCAACCTCTGCCCTCAGGTT 4018
 AAGTGATTCTCCTGCCCTCAGCTCCCTGAGTAGCTAGGATTAGAGGCATGCCCCAACAC 4078
 CTGGCTAACCTCTGTTACAGAGATGAGGTTTACCATGTTGGTGGCTGGCTGGTGC 4138
 TGAACCTCTGACCTGGTGTGATCTGCCACCTCAGCCTCCAAAGTACTGGGATGACAGGCA 4198
 TGAACCACGTGCTGGCCATCTTTTTATTAAAGAGATGGTTCTGCTAAGTTGC 4258
 CCAGAGCGAGTTAATTTCAGGCTGGCTCAAGTAATCTTCACCTAGTCTCTGGTAGCT 4318
 GCAACCAAGGCACCCGGTTATCTGCAATTCTCTTTCTTGTAGAGCTGAGTCTG 4378
 TCTGTAGCCCAGGCTGGAGCGCAGTGGCGTGTACTGCAACCTCCCTCTCA 4438
 GGGTCAAGCAATTCTCTGCCCTCAGCCTCTGGAGTGGCTGGACTACAGGGCTGTGCCA 4498
 CCAGAGCGAGTTAATTTCAGGCTGGCTCAAGTAATCTTCACCTAGTCTCTGGTAGCT 4558
 TTGGCCAGGCTGGCTTGACTCTGACCTCAAGTGTACGCCCTGCCCTGGCTCCAAA 4618
 GTGCTGGGATTACAGGCACAGGCGTGAGCCACTACACCTGGCTATCTGCAATTCTCTAA 4678
 TAGTTCTTAGAAATGGATTCTTAGGAGTAGGATTACACAGTCAGAGAGACACAAGTTTG 4738
 TAGGCTGGGCTGGCTGGACTCTGACCTCAAGTGTACGCCCTGCCCTGGCTCCAAA 4798
 TGGGAGGCTGGGGTGGAGGATCAATTGAGCCCAGGGTGTGGTGTGCTGTAGCTTAC 4918
 TTAGGAGGCTGGGGTGGAGGATCAATTGAGCCCAGGGTTAGAGCTGAGCTGAGCTGT 4978
 GATTGCACCATGGCACTCCACCCCTGGGCTCAAAGTGTAGGATCTGCTCCAAACAAAAA 5038
 AGATACAAGTATCTTAAAGGCTCTGCTACACATGCCAGGAAGGTAGTCTATTGGACAG 5098
 TTTTAAGTCATTATCAATTAGCTCATTTAATTCCCTCCAAALACTCTGTAAAGCACAT 5158
 TCTGCTACCATAGTTGCAATTATTTGATGGGGAACTACACTGAGAGGCAGTGTGGG 5218
 ATCTGAACCCCATCTTAAAGATTAGCTCAGGGCCATGCTTGTACTGGCTGGCCGG 5278
 CTGCCCCACACTGAGTGTGTTCTCTGAGGGTAGGTGTGCTATCTCAGGGACACTAG 5338
 ACAGCTCCGAGGGACCTCCCTGCTCTGTCAGATGCCCTGGCCAAAGGTTTACACTG 5398
 AGGGCTCAGACCTGCCCTGCCCTCTGTCAGATGCCCTGGCCAAAGGTTTACACTG 5458
 GAACAAGTTGGTCCCTCTCCCCACCCAGGCTGTCTGGCCCTCTCCAGGTCTCCTT 5518

FIGURE 2(c)

INTERNATIONAL SEARCH REPORT

International application No
PCT/US95/06743

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 5/10, 9/12, 15/54, 15/63, 15/85; C12Q 1/00, 1/68, C07K 16/40
US CL : 435/6, 7.1, 194, 240.1, 320.1, 536/23.2, 530/388.26.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 7.1, 194, 240.1, 320.1, 536/23.2, 530/388.26;

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Computer Search - CA, APS, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No |
|-----------|--|----------------------|
| A | Biochimica Biophysica Acta, Volume 831, issued 1985, D. Stambolian, et. al., "Purification Of Human Galactokinase And Evidence For Its Existence As A Monomer Form", Pages 306-312, see entire document.' | 1-21 |
| A | Proc. Natl. Acad. Sci., USA, Volume 89, issued November 1992, R. T. Lee, et. al., "Cloning Of A Human Galactokinase Gene (GK2) On Chromosome 15 By Complementation In Yeast", pages 10,887-10,891, see entire document | 1-21 |
| A | Nucl. Acids Res., Volume 13, No. 6, issued 1985, C. Debouck, et. al., "Structure Of The Galactokinase Gene Of Escherichia Coli, The Last (?) Gene Of The Gal Operon", pages 1841-1853, see entire document. | 1-21 |

Further documents are listed in the continuation of Box C.

See patent family annex.

| | | |
|--|---|---|
| * Special categories of cited documents: | *T* | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| *A* | document defining the general state of the art which is not considered to be of particular relevance | |
| *E* | earlier document published on or after the international filing date | |
| *L* | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | *X* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| *O* | document referring to an oral disclosure, use, exhibition or other means | *Y* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| *P* | document published prior to the international filing date but later than the priority date claimed | *& document member of the same patent family |

Date of the actual completion of the international search

03 AUGUST 1995

Date of mailing of the international search report

31 AUG 1995

Name and mailing address of the ISA/US
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Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No
PCT/US95/06743

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No |
|-----------|---|----------------------|
| A | Mol. Microbiol., Volume 10, No. 2, issued 1993, P. Glaser, et al., "Bacillus Subtilis Genome Project: Cloning And Sequencing Of The 97 kb Region From 325 degrees to 333 degrees", pages 371-384, see entire document. | 1-21 |
| A | J. Bacteriol., Volume 172, No. 8, issued August 1990, H. H. Houng, et. al., "Molecular Cloning And Physical And Functional Characterization Of The Salmonella Typhimurium and Salmonella Typhi Galactose Utilization Operons", pages 4392-4398, see entire document | 1-21 |

INTERNATIONAL SEARCH REPORT

International application No

PCT/US95/06743

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos..

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos..

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application N
PCT/US95/06743

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claims 1-8 and 21, drawn to nucleic acid, a vector containing the nucleic acid, a host cell containing the vector and a method of use.

Group II, claim 9, drawn to human galactokinase.

Group III, claims 10-11, drawn to an antibody and a method of use.

Group IV, claims 12-20, drawn to a method of diagnosing conditions associated with human galactokinase deficiency using a nucleic acid.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The nucleic acid, vector, host cell and method of use of Group I involve separate and distinct chemical compounds from the enzyme of Group II and antibody of Group III, and therefore Groups I-III do not share a special technical feature. The method of use of the nucleic acid in Group I, namely to prepare a galactokinase protein, is a separate and distinct use from the use of the nucleic acid to diagnose galactokinase deficiencies of Group IV and therefore Groups I and IV do not share a special technical feature. Accordingly, the claims are not so linked as to form a single general inventive concept.